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OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 17:43:54 ; Search time 325 Seconds
(without alignments)
6538.363 Million cell updates/sec

Title: US-09-508-745-3

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Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	526.6	90.6	583	9	US-09-925-674A-6
3	375.6	64.6	1864	10	US-09-809-391-130
4	375.6	64.6	1864	10	US-09-882-171-130
5	375.4	64.6	578	14	US-10-029-386-10549
6	374.4	64.4	433	14	US-10-029-386-24249
7	221.8	38.2	6049	14	US-10-311-455-201
8	194.2	33.4	6049	14	US-10-311-455-201
9	148.4	25.5	151	14	US-10-029-386-27084
10	148.4	25.5	350	14	US-10-029-386-13384
11	147.4	25.4	150	9	US-09-864-761-17690
12	141.2	24.3	540	15	US-10-402-017-5
13	140.4	24.2	660	15	US-10-402-017-9
14	137.8	23.7	600	15	US-10-402-017-7
15	133	22.9	636	14	US-10-169-223-13

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17	133	22.9	702	10	US-09-959-987-9	Sequence 9, Appl
18	133	22.9	863	15	US-10-402-017-3	Sequence 3, Appl
19	133	22.9	926	9	US-09-734-846-1	Sequence 1, Appl
20	133	22.9	926	9	US-09-734-847A-39	Sequence 39, Appl
21	133	22.9	926	9	US-09-952-278-5	Sequence 5, Appl
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24	133	22.9	926	15	US-10-402-017-1	Sequence 1, Appl
25	125.2	21.5	600	9	US-09-864-761-7360	Sequence 7360, Ap
26	124.2	21.4	492	10	US-09-918-995-33305	Sequence 33305, A
27	124.2	21.4	555	9	US-09-864-761-24081	Sequence 24081, A
28	124.2	21.4	564	14	US-10-029-386-20790	Sequence 20790, A
29	121.8	21.0	717	14	US-10-053-645A-20	Sequence 20, Appl
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31	121.8	21.0	5086	14	US-08-726-211-4	Sequence 4, Appl
32	121.8	21.0	5086	14	US-10-141-618-11	Sequence 11, Appl
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34	121.8	21.0	6030	14	US-10-171-581-187	Sequence 187, App
35	121.8	21.0	6030	14	US-10-007-926A-117	Sequence 117, App
36	121.8	21.0	6142	14	US-10-198-846-13703	Sequence 13703, A
37	120.2	20.7	1303	9	US-09-952-278-1	Sequence 1, Appl
38	120.2	20.7	1748	15	US-10-388-934-539	Sequence 539, App
39	120.2	20.7	1748	15	US-10-191-803-202	Sequence 202, App
40	117.4	20.2	615	14	US-10-053-645A-22	Sequence 22, Appl
41	117.4	20.2	911	8	US-08-726-211-6	Sequence 6, Appl
42	117.4	20.2	911	15	US-10-387-961A-6	Sequence 6, Appl
43	117.4	20.2	911	15	US-10-402-017-2	Sequence 2, Appl
44	114	19.6	1384	14	US-10-208-155-1	Sequence 1, Appl
45	94.4	16.2	439	9	US-09-864-761-912	Sequence 912, App

ALIGNMENTS

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RESULT 1
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; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 116864
; CURRENT APPLICATION NUMBER: US/09/925, 674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925, 674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P08965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8

Query Match          99.4%; Score 577.8; DB 9; Length 582;
Best Local Similarity 99.7%; Pred. No. 1.5e-157;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 6, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
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; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-6

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Best Local Similarity 94.1%; Pred. No. 16-142;
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RESULT 3
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; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; PRIOR FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,c,g, or c
US-09-809-391-130

Query Match 64.6%; Score 375.6; DB 10; Length 1864;
Best Local Similarity 91.7%; Pred. No. 6-9e-99;
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;
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 ; Sequence 130, Application US/09882171
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 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/882,171
 ; CURRENT FILING DATE: 2001-06-18
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Best Local Similarity 91.7%; Pred. No. 6.9e-99;
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;
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DB 251 CAGGTTTCCAGTAACTTTTCAAGGGGGCCCCAACTGGGCGCTTGTGTGATTTT 310
QY 301 GTCTTTGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGGTGG 360
DB 311 GTCTTTGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGGTGG 370
QY 361 CAAGTGCAGATTGGATGTGGCTTACCTGTGAGACACCTGTGCTGTGATGTGATCCAGC 420
DB 371 CAAGTGCAGAGTGTGATGTGGCTTACCTGTGAGAGAGCGGCTGTGATGTGATCCAGC 430
QY 421 AGTGGGGGCTGG 432
DB 431 AGTGGGGGCTGG 442
RESULT 5
US-10-029-386-10549
; Sequence 10549, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10549
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALU8 0.00e+00
; OTHER INFORMATION: NT HIT: gi14751151, EVALU8 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALU8 2.00e-72
US-10-029-386-10549
Query Match 64.6%; Score 375.4; DB 14; Length 578;
Best Local Similarity 91.7%; Pred. No. 6.7e-99;

Matches 397; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

DB 105 ATGGCGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 164

QY 61 AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCGCGAC 120

DB 165 AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCGCTGAC 224

QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACGAGTTTGAAGCCCGTTTCCGCGAC 180

DB 225 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGATGAGTTTGAAGCCCGTTTCCGCGAC 284

QY 181 TTCTCTGACCTGGCCGCTCACTACGTACGCCAGGCTAGCCCAAGAGCTTCAAC 240

DB 285 TTCTCTGACCTGGCCGCTCACTACGTACGCCAGGCTAGCCCAAGAGCTTCAAC 344

QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTTGTGGCAATCTTT 300

DB 345 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTTGTGGCAATCTTT 404

QY 301 GTCTTTGGGGCTGCTGTGTGTGAGAGTCAAAAGAAATGAGCCTTTGTGGGGA 360

DB 405 GTCTTTGGGGCTGCACTGTGTGTGAGAGTCAAAAGAGATGGAACCACTGTGGGA 464

QY 361 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGACAGCTGTGCTGACTGATCCAGC 420

DB 465 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGACAGCTGTGCTGACTGATCCAGC 524

QY 421 AGTGGGGGCTGG 433

DB 525 AGTGGGGGCTGG 537

RESULT 6

US-10-029-386-24249

; Sequence 24249, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AECOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029.386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 24249

; LENGTH: 433

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR14.3

; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.2

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2

; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUOE 0.00e+00

; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUOE 2.00e-72

; OTHER INFORMATION: NT HIT: g14751151, EVALUOE 0.00e+00

US-10-029-386-24249

Query Match 64.4%; Score 374.4; DB 14; Length 433;

Best Local Similarity 91.7%; Pred. No. 1.2e-98;

Matches 396; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

DB 2 ATGGCGACCCCAAGCTTCAACCCAGACACAGGGCTCTGATGGAGACTTTGTAGTAT 61

QY 61 AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCGCGAC 120

DB 62 AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCGCTGAC 121

QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGACGAGTTTGAAGCCCGTTTCCGCGAC 180

DB 122 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGATGAGTTTGAAGCCCGTTTCCGCGAC 181

QY 181 TTCTCTGACCTGGCCGCTCACTACGTACGCCAGGCTAGCCCAAGAGCTTCAAC 240

DB 182 TTCTCTGACCTGGCCGCTCACTACGTACGCCAGGCTAGCCCAAGAGCTTCAAC 241

QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTTGTGGCAATCTTT 300

DB 242 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAAGTGGGGCGCTTTGTGGCAATCTTT 301

QY 301 GTCTTTGGGGCTGCTGTGTGTGAGAGTCAAAAGAAATGAGCCTTTGTGGGGA 360

DB 302 GTCTTTGGGGCTGCACTGTGTGTGAGAGTCAAAAGAGATGGAACCACTGTGGGA 361

QY 361 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGACAGCTGTGCTGACTGATCCAGC 420

DB 362 CAAGTGCAGAGTTGATGTGTGCTTACCTGAGACAGCTGTGCTGACTGATCCAGC 421

QY 421 AGTGGGGGCTGG 432

DB 422 AGTGGGGGCTGG 433

RESULT 7

US-10-311-455-201

; Sequence 201, Application US/10311455

; Publication No. US20030143606A1

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

; APPLICANT: PIEPENBROCK, Christian

; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

; FILE REFERENCE: 5013.1014

; CURRENT APPLICATION NUMBER: US/10/311.455

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: PCT/EP01/07537

; PRIOR FILING DATE: 2001-07-02

; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: DE 10043826.1

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 2424

; SEQ ID NO 201

; LENGTH: 6049

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-201

Query Match 38.2%; Score 221.8; DB 14; Length 6049;

Best Local Similarity 69.5%; Pred. No. 3e-54;

Matches 301; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCAAGCTTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

DB 5001 ATGGCGATTTTATGTTTGATTTAGATATACGGGTTTGGTGTGATTTTGTATGTTAT 5060

QY 61 AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCGCGAC 120

DB 5061 AAGTTGAGGTGAAGAGGGTTATGTCTGTGAGAGTGGTTCCGGGAGGGGTTTATGATGTTAT 5120

QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGAGACGAGTTTGAAGCCCGTTTCCGCGAC 180

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Db 5121 TCGTGTATTAGTATATGCGGGTAGTGGAGATGAGTTCGATTGTTTCGGGTATT 5180
Qy 181 TTCTGACCTTGGCCGCTAGCTACACGTCGACCCAGAGCTCAGCCAGAACGCTTCACC 240
Db 5181 TTTTGTGATTTGGCGGTAGTGTATGATGATTTAGTGTATTAATTAAGTGTATTAT 5240
Qy 241 CAGTTTTCGACGAATTTTCCAAAGGGGACCTTAACCTGGGGCCGCTTGTGGCATTCTTT 300
Db 5241 TAGGTTTTCGATGAATTTTAAAGGGGCTTTAAATGGGCGTTCGTTTGTATTTT 5300
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGCA 360
Db 5301 GTTTTGGGGGTGTATGTTGTGTGAGAGTGTAAATAGAGAGATGGAATTTATGGTGGCA 5360
Qy 361 CAAGTCGACGATTTGATGTGGCTACCTCGAGACACGCTTCGACCTGATCCACAGC 420
Db 5361 TAAAGTGTAGAGATGTGATGTGTATTATTTAGAGACGTAAGTGTGATTGATTTAATAGT 5420
Qy 421 AGTGGGGGCTGGG 433
Db 5421 AGTGGGGGCTGGG 5433

RESULT 8
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 1002529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

Query Match 33.4%; Score 194.2; DB 14; Length 6049;
Best Local Similarity 66.2%; Pred. No. 3e-46;
Matches 280; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 1 AATGGGACCCCAAGCTTCAACCCCAAGACAGAGGCGCTAGTGGCTTGTAGGCTAT 60
Db 1049 ATTAAGACCCCAAGCTTCAACCCCAAGACAGAGCTTCAATTAACAACTTTAATAATAT 990
Qy 61 AAGCTGAGGACAGAGGGTATGTCTGTGAGCTGGCCCTGGGAGAGCCAGCCGCCGAC 120
Db 989 AAACCTAAACCAAAAAATTAATATCTATAAACTAACCCGAAAAAACCAACAATAAC 930
Qy 121 CCGCTGACCAAGCAATGCGGGCTGTGAGACGAGTTTGAAGCCGTTTCGCCGCAC 180
Db 929 CCGCTACACCAACCAATGAGCACTAATAAATAATTTGAATCCGCTTCGAGACGAC 870
Qy 181 TTCTGACCTGCGCGCTAGCTACACGTCGACCCCAAGGCTGAGCCAGAACGCTTAC 240
Db 869 TTCTCTAAATCTAACGATCACTACATATTAACCCCAACCAACCAAGCTTAC 810
Qy 241 CAGGTTTCCGACGAATTTTCAAGGGGCGCTTAAGTGGGCGCTTGTGCAATTTCT 300
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Db 809 CAATCTCCGATTAACCTTTTCAAAAAAACCACCTAATAACCGCTTATTAACCTTCTTT 750
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGCA 360
Db 749 ATCTTAAACTACACTATATACCTAATAATATCAACAAAAATTAACCACTAATAATA 690
Qy 361 CAAGTCGACGATTTGATGTGGCTTACCTCGAGACACGCTGTGCTGATCGATCCACAGC 420
Db 689 CAATACCAAAAAATTAATAATTAACCTACTAATAAACGCAACTAATTAATCAACAG 630
Qy 421 AGT 423
Db 629 AAT 627

RESULT 9
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: A6OMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 5.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
; OTHER INFORMATION: NT HIT: g14574571, EVALUE 9.00e-80
US-10-029-386-27084

Query Match 25.5%; Score 148.4; DB 14; Length 151;
Best Local Similarity 99.3%; Pred. No. 3.3e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 432 GCGGAGTTCAAGCTCTATACGGGACGCGGCCCTGAGAGGACGCGCTTGGCGGA 491
Db 1 GCGGAGTTCAAGCTCTATACGGGACGCGGCCCTGAGAGGCGCGCGCTTGGCGGA 60
Qy 492 GGGGACCTGGGATCAGTGAAGACAGTCTCAACGGGGGCGGTGACACTGGGGGCGCTGT 551
Db 61 GGGGACCTGGGATCAGTGAAGACAGTCTCAACGGGGGCGGTGACACTGGGGGCGCTGT 120
Qy 552 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 121 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 150

RESULT 10
US-10-029-386-13384
; Sequence 13384, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: A6OMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
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NUMBER OF SEQ ID NOS: 3428
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13384
LENGTH: 590
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHRI4.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10
OTHER INFORMATION: NT HIT: G14751151, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 1.00e-119
US-10-029-386-13384

Query Match      25.5%; Score 148.4; DB 14; Length 590;
Best Local Similarity 99.3%; Pred. No. 4e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 432 GCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAGAGGACGGCGTTCGGGGA 491
Db 25 GCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAGAGGACGGCGTTCGGGGA 84
Qy 492 GGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 551
Db 85 GGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 144
Qy 552 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 145 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 174

RESULT 11
US-09-864-761-17690
Sequence 17690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmeca-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US/09/864,761
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17690
LENGTH: 150
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049829.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79
OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 8.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
US-09-864-761-17690

Query Match      25.4%; Score 147.4; DB 9; Length 150;
Best Local Similarity 99.3%; Pred. No. 6.3e-33;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 433 GCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAGAGGACGGCGTTCGGGAG 492
Db 1 GCGGAGTTCAAGCTCTATACGGGAGCGGGCCCTGGAGAGGACGGCGTTCGGGAG 60
Qy 493 GGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 552
Db 61 GGGGAAGTGGGCAATGAGAGACAGTGTGACGGGGCCGTGGCACTGGGGCCCTGCT 120
Qy 553 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
Db 121 AACTGTAGGGGCTTTTGTGCTAGCAAGTG 149

RESULT 12
US-10-402-017-5
Sequence 5, Application US/10402017
Publication No. US20030219871A1
GENERAL INFORMATION:
APPLICANT: Barbara ENNEKEL, Heiko MEENTS and Martin FUSSENDEGER
TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
FILE REFERENCE: Case 1/1314
CURRENT FILING DATE: 2003-03-28
PRIORITY APPLICATION NUMBER: US/10/402,017
PRIORITY FILING DATE: 2003-03-28
PRIORITY APPLICATION NUMBER: US 60/369,307
PRIORITY APPLICATION NUMBER: April 2, 2002
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 540
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del26-83)
US-10-402-017-5

Query Match      24.3%; Score 141.2; DB 15; Length 540;
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QY 388 CTGGAGACAGTCTGGCTGACTGATCCAGCAGTGGGGGCTGGGGAGTTGACAGCT 447
Db 418 CTGAATATACCACTTAGAGCTTTGATCCAGACAGCGGCTGGACATTTGTGTGAA 477
QY 448 CTATACGGGGACGGGGCCCTGGAGAGGACAGCGCTCTGCGGAGGGGAACTGGGCATCA 507
Db 478 CTTACCGGAAACATATGACAGCTGAGAGCCGGAAAGGCCAGAGCGCTTCAACCGCTGG 537
QY 508 GTGAGGACAGTGTGACCGGGGGCCG 532
Db 538 TTCCTGACGGGCATGACTGTGGCTG 562

RESULT 15
US-10-169-223-13

/ Sequence 13, Application US/10169223
/ Publication No. US20030152946A1
/ GENERAL INFORMATION:
/ APPLICANT: SHIMIZU, Shigeomi
/ APPLICANT: TSUJIMOTO, Yoshihide
/ TITLE OF INVENTION: BH4-Fused Polypeptides
/ FILE REFERENCE: 1422-0537P
/ CURRENT APPLICATION NUMBER: US/10/169,223
/ CURRENT FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: JP 11-371449
/ PRIOR FILING DATE: 1999-12-27
/ PRIOR APPLICATION NUMBER: PCT/JP00/09274
/ PRIOR FILING DATE: 2000-12-26
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 13
/ LENGTH: 636
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized DNA for mutant bcl-xl
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(636)
/ OTHER INFORMATION:
US-10-169-223-13

Query Match 22.9%; Score 133; DB 14; Length 636;
Best Local Similarity 58.0%; Pred. No. 1.2e-28;
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCATCGGGCTGCTGAGACGAGTTTGAGACCCGTTCCGCCGACCTTCTCTG 187
Db 197 AGCAAGCGCTGAGAGGAGGAGCGAGGATTGAACTGGGTACCGGCGGCGATTCAGTG 256
QY 188 ACCTGGCCGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTCAACCCAGTGT 247
Db 257 ACCTGACATCCAGTCCATCAATCCAGGACAGCATATCAGAGCTTTGAACAGGTAG 316
QY 248 CCGACGAACTTTCCAGGGGGCCCTAACTGGGGCCGTTCTGTGGCATTTCTTGTCTTG 307
Db 317 TGAATGAACCTTCGGGATGGGGTAACTGGGGTGGCATTTGTGCTTCTTCG 376
QY 308 GGGCTGCCCTGTCGTGAGAGTGCACAAAGAAATGAGCCTTTGGTGGGACAAGTGC 367
Db 377 GCGGGGCACTGTGCTGGAAGCGTGAAGAGAGATCAGGTATTTGGTGGATCGATCG 436
QY 368 AGAATTGATGATGCTTACTGAGACAGCTGTGGTGAATCCACAGCAGTGGGG 427
Db 437 CAGCTTGGATGGCCACTTAACCTGAATGACACTTAGAGCTTTGATCCAGGAGAACGGCG 496
QY 428 GCTGGCGGAGTTTCAAGCTTATACGGGGACGGGGCCCTGGAGGAGCAGGCGTCTGC 487
Db 497 GCTGGATATCTTTGTGGAACCTATGGGAACAATGACAGCCGAGAGCCGAAAGGGCC 556
QY 488 GGGAGGGGACATGGGCACTGAGGAGACAGTGTGCTGACGGGGGCG 532

Db 557 AGAAGCCTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCCG 601

Search completed: March 3, 2004, 19:53:48
Job time : 330 secs

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us-09-508-745-3.rge

Bertog 110
091508745 Page 1
Seq 105 374

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query	Description
No	Watch	TP

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	AY185100	Kalcus I
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565	1110	AY185100
5	97.2	10
565	3487	AY185098
		Battus I

Seq	Length	Score	Seq	Length	Score
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7	561.4	96.6	579	6	AR020779

Order	Quantity	Unit Price	Amount	Description
8	580.2	38.4	22089.6	Sequence
9	560.2	96.4	53981.28	AX030819 Sequence

	U59747	Human Bcl-2
11	526.6	90.6
11	582	9

13	521.8	89.8	583	6	AX022529	AX022529 Sequence
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15	518.2	89.2	579	6	AR020780	AR020780 Sequence
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Accession	Length (bp)	GC (%)	GC (20-30 bp)	GC (30-40 bp)	GC (40-50 bp)	GC (50-60 bp)	GC (60-70 bp)	GC (70-80 bp)	GC (80-90 bp)	GC (90-100 bp)	GC (100-110 bp)	GC (110-120 bp)	GC (120-130 bp)	GC (130-140 bp)	GC (140-150 bp)	GC (150-160 bp)	GC (160-170 bp)	GC (170-180 bp)	GC (180-190 bp)	GC (190-200 bp)	GC (200-210 bp)	GC (210-220 bp)	GC (220-230 bp)	GC (230-240 bp)	GC (240-250 bp)	GC (250-260 bp)	GC (260-270 bp)	GC (270-280 bp)	GC (280-290 bp)	GC (290-300 bp)	GC (300-310 bp)	GC (310-320 bp)	GC (320-330 bp)	GC (330-340 bp)	GC (340-350 bp)	GC (350-360 bp)	GC (360-370 bp)	GC (370-380 bp)	GC (380-390 bp)	GC (390-400 bp)	GC (400-410 bp)	GC (410-420 bp)	GC (420-430 bp)	GC (430-440 bp)	GC (440-450 bp)	GC (450-460 bp)	GC (460-470 bp)	GC (470-480 bp)	GC (480-490 bp)	GC (490-500 bp)	GC (500-510 bp)	GC (510-520 bp)	GC (520-530 bp)	GC (530-540 bp)	GC (540-550 bp)	GC (550-560 bp)	GC (560-570 bp)	GC (570-580 bp)	GC (580-590 bp)	GC (590-600 bp)	GC (600-610 bp)	GC (610-620 bp)	GC (620-630 bp)	GC (630-640 bp)	GC (640-650 bp)	GC (650-660 bp)	GC (660-670 bp)	GC (670-680 bp)	GC (680-690 bp)	GC (690-700 bp)	GC (700-710 bp)	GC (710-720 bp)	GC (720-730 bp)	GC (730-740 bp)	GC (740-750 bp)	GC (750-760 bp)	GC (760-770 bp)	GC (770-780 bp)	GC (780-790 bp)	GC (790-800 bp)	GC (800-810 bp)	GC (810-820 bp)	GC (820-830 bp)	GC (830-840 bp)	GC (840-850 bp)	GC (850-860 bp)	GC (860-870 bp)	GC (870-880 bp)	GC (880-890 bp)	GC (890-900 bp)	GC (900-910 bp)	GC (910-920 bp)	GC (920-930 bp)	GC (930-940 bp)	GC (940-950 bp)	GC (950-960 bp)	GC (960-970 bp)	GC (970-980 bp)	GC (980-990 bp)	GC (1000-1010 bp)	GC (1010-1020 bp)	GC (1020-1030 bp)	GC (1030-1040 bp)	GC (1040-1050 bp)	GC (1050-1060 bp)	GC (1060-1070 bp)	GC (1070-1080 bp)	GC (1080-1090 bp)	GC (1090-1100 bp)	GC (1100-1110 bp)	GC (1110-1120 bp)	GC (1120-1130 bp)	GC (1130-1140 bp)	GC (1140-1150 bp)	GC (1150-1160 bp)	GC (1160-1170 bp)	GC (1170-1180 bp)	GC (1180-1190 bp)	GC (1190-1200 bp)	GC (1200-1210 bp)	GC (1210-1220 bp)	GC (1220-1230 bp)	GC (1230-1240 bp)	GC (1240-1250 bp)	GC (1250-1260 bp)	GC (1260-1270 bp)	GC (1270-1280 bp)	GC (1280-1290 bp)	GC (1290-1300 bp)	GC (1300-1310 bp)	GC (1310-1320 bp)	GC (1320-1330 bp)	GC (1330-1340 bp)	GC (1340-1350 bp)	GC (1350-1360 bp)	GC (1360-1370 bp)	GC (1370-1380 bp)	GC (1380-1390 bp)	GC (1390-1400 bp)	GC (1400-1410 bp)	GC (1410-1420 bp)	GC (1420-1430 bp)	GC (1430-1440 bp)	GC (1440-1450 bp)	GC (1450-1460 bp)	GC (1460-1470 bp)	GC (1470-1480 bp)	GC (1480-1490 bp)	GC (1490-1500 bp)	GC (1500-1510 bp)	GC (1510-1520 bp)	GC (1520-1530 bp)	GC (1530-1540 bp)	GC (1540-1550 bp)	GC (1550-1560 bp)	GC (1560-1570 bp)	GC (1570-1580 bp)	GC (1580-1590 bp)	GC (1590-1600 bp)	GC (1600-1610 bp)	GC (1610-1620 bp)	GC (1620-1630 bp)	GC (1630-1640 bp)	GC (1640-1650 bp)	GC (1650-1660 bp)	GC (1660-1670 bp)	GC (1670-1680 bp)	GC (1680-1690 bp)	GC (1690-1700 bp)	GC (1700-1710 bp)	GC (1710-1720 bp)	GC (1720-1730 bp)	GC (1730-1740 bp)	GC (1740-1750 bp)	GC (1750-1760 bp)	GC (1760-1770 bp)	GC (1770-1780 bp)	GC (1780-1790 bp)	GC (1790-1800 bp)	GC (1800-1810 bp)	GC (1810-1820 bp)	GC (1820-1830 bp)	GC (1830-1840 bp)	GC (1840-1850 bp)	GC (1850-1860 bp)	GC (1860-1870 bp)	GC (1870-1880 bp)	GC (1880-1890 bp)	GC (1890-1900 bp)	GC (1900-1910 bp)	GC (1910-1920 bp)	GC (1920-1930 bp)	GC (1930-1940 bp)	GC (1940-1950 bp)	GC (1950-1960 bp)	GC (1960-1970 bp)	GC (1970-1980 bp)	GC (1980-1990 bp)	GC (2000-2010 bp)	GC (2010-2020 bp)	GC (2020-2030 bp)	GC (2030-2040 bp)	GC (2040-2050 bp)	GC (2050-2060 bp)	GC (2060-2070 bp)	GC (2070-2080 bp)	GC (2080-2090 bp)	GC (2090-2100 bp)	GC (2100-2110 bp)	GC (2110-2120 bp)	GC (2120-2130 bp)	GC (2130-2140 bp)	GC (2140-2150 bp)	GC (2150-2160 bp)	GC (2160-2170 bp)	GC (2170-2180 bp)	GC (2180-2190 bp)	GC (2190-2200 bp)	GC (2200-2210 bp)	GC (2210-2220 bp)	GC (2220-2230 bp)	GC (2230-2240 bp)	GC (2240-2250 bp)	GC (2250-2260 bp)	GC (2260-2270 bp)	GC (2270-2280 bp)	GC (2280-2290 bp)	GC (2290-2300 bp)	GC (2300-2310 bp)	GC (2310-2320 bp)	GC (2320-2330 bp)	GC (2330-2340 bp)	GC (2340-2350 bp)	GC (2350-2360 bp)	GC (2360-2370 bp)	GC (2370-2380 bp)	GC (2380-2390 bp)	GC (2390-2400 bp)	GC (2400-2410 bp)	
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[illegible]

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44	133.4	23.0	2232	10	RNCBLXLS	X82537 R.norvegicus
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ALIGNMENTS

RESULT 1

MMU59746	582 bp	MRNA	linear	ROD 29-SEP-19
LOCUS				
MMU59746				

DEFINITION	MUS MUSCULUS DCL-W (DCL-W/ INACTV, COMPLETE CUS:
ACCESSION	U59746

KEYWORDS

ORGANISM	Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

AUTHORS Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,

TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival

no motivation

JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson, L., Holmgren, S. P., Huang, D. C. S., Bernard, O., Adams, J. M. and Cory, S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
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DB 541 GGGGCGCTGTAACTGTAGGGCGCTTTTGTGTAAGCAAGT 581
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AF030769
LOCUS AF030769 3476 bp mRNA linear ROD 16-NOV-1997
DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION AF030769
VERSION AF030769.1 GI:2623249
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3476)
Ross, A. J., Maymire, K. G., Moss, J. E., Parlow, A. F., Russell, L. D. and MacGregor, G. R.
Bcl-w is required for testis homeostasis
TITLE Unpublished
JOURNAL 2 (bases 1 to 3476)
REFERENCE Rose, A. J. and MacGregor, G. R.
TITLE Direct Submission
AUTHORS Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA
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Best Local Similarity 100.0%; Pred. No. 4.3e-131;
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DB 179 ATGGGACCCCAAGCTTATGCTGAGAGTGGGCTCTAGTGGCTTGTAGGCTAT 238
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Oy	121	CCGCTGCACCAAGCCATCCGAGGCTGCTGAGAGCGAGTTTGAGACCCGTTTCCGCCGACC	180
Db	299	CCGCTGCACCAAGCCATCCGAGGCTGCTGAGAGCGAGTTTGAGACCCGTTTCCGCCGACC	358
Oy	181	TTCTCTGACCTGGCCGCTCAGTTACACGTGAACCCAGGCTACGCCACGACAGCTTTCAC	240
Db	359	TTCTCTGACCTGGCCGCTCAGTTACACGTGAACCCAGGCTACGCCACGACAGCTTTCAC	418
Oy	241	CAGGTTTCCGACGAACTTTTCCAAAGGAGGCCCTTAACGTGAGGCCGCTTGTGGCACTTCTT	300
Db	419	CAGGTTTCCGACGAACTTTTCCAAAGGAGGCCCTTAACGTGAGGCCGCTTGTGGCACTTCTT	478
Oy	301	GTCTTTGGAGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGACCTTTGTGTGGA	360
Db	479	GTCTTTGGAGGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGACCTTTGTGTGGA	538
Oy	361	CAAGTGCAGAATTGGATGTGTGGCTTAACCTGAGAGACAGCTCTGTGCTGACTGATTCACAGC	420
Db	539	CAAGTGCAGAATTGGATGTGTGGCTTAACCTGAGAGACAGCTCTGTGCTGACTGATTCACAGC	598
Oy	421	AGTGGAGGACTGAGGCGGAGTTCAACAGCTCTATACCGGAGACGGGGCCCTGTGAGAGGACACGG	480
Db	599	AGTGGAGGACTGAGGCGGAGTTCAACAGCTCTATACCGGAGACGGGGCCCTGTGAGAGGACACGG	658
Oy	481	CGTCTGCGGAGAGGGAGCAATGGGCATCACTGAGAGACAGTGTGACCGGAGGCCGTGTGCACTG	540
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Oy	541	GGGGCCCTGTGTACTGTAGGGGCTTTTTTGTGTACCAAGTG	581
Db	719	GGGGCCCTGTGTACTGTAGGGGCTTTTTTGTGTACCAAGTG	759

RESULT 3	AF096291	582 bp	mRNA	linear	ROD 28-FEB-2000
LOCUS	AF096291				
DEFINITION	Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.				
ACCESSION	AF096291				
VERSION	AF096291.1	GI:3747129			
KEYWORDS					
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 582)				
AUTHORS	Hammer,S., Skoglosa,Y. and Lindholm,D.				
TITLE	Differential expression of bcl-w and bcl-x messenger RNA in the				
	developing and adult rat nervous system				
JOURNAL	Neuroscience 91 (2), 673-684 (1993)				
MEDLINE	99392146				
PUBMED	10366024				
REFERENCE	2 (bases 1 to 582)				
AUTHORS	Hammer,S., Skoglosa,Y. and Lindholm,D.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala				
	University, Box 587, BMC, Uppsala 751 23, Sweden				
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Query Match	97.2%	Score 565	DB 10	Length 582	
Best Local Similarity	98.3%	Pred. No. 4,2e-127			
Matches 571	Conservative 0	Mismatches 10	Indels 0	Gaps 0	
QY	1	ATGGCGA	CCCCAGCCTCA	CCCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGCTAT	60
Db	1	ATGGCGA	CCCCAGCCTCA	CCCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGCTAT	60
QY	61	AAGCTGAGG	CAGAAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCAGCCGGCAGC	120	
Db	61	AAGCTGAGG	CAGAAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAAGGCCAGCCAGCCGAC	120	
QY	121	CCGCTGCAC	CAAGGCATACGGGCTGTGAGAGCAGATTGTGAGACCCGCTTTCGGCGCAC	180	
Db	121	CCGCTGCAC	CAAGGCATACGGGCGACGCTGGAGACGAGTTTGAAGACCGCTTTCGGGCGCAC	180	
QY	181	TTCTCTGAC	CTGGCCGCTCAGCTACACGCTGACCCCGAGCTTACGCCAGCAACGCTTACC	240	
Db	181	TTCTCTGAC	CTGGCCGCTCAGCTACACGCTGACCCCGAGCTTACGCCAGCAACGCTTACC	240	
QY	241	CAGGTTTCC	CAAGCAACTTTTCCAAAGGGGGCCCTTAACCTGGGGCGCTTTGTGGCAATTCTTT	300	
Db	241	CAGGTTTCC	CAAGCAACTTTTCCAAAGGGGGCCCAACTGGGGCGCTTTGTGGCAATTCTTT	300	
QY	301	GTCTTTTGG	GGCTGCTCTGTGTCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA	360	
Db	301	GTCTTTTGG	GGCTGCTCTGTGTCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA	360	
QY	361	CAAGTGCAG	ATTGGATGTGTGGCTTACTTGGAGACACGCTGTGGCTGACTGATTCACACGC	420	
Db	361	CAAGTGCAG	ATTGGATGTGTGGCTTACTTGGAGACACGCTGTGGCTGACTGATTCACACGC	420	
QY	421	AGTGGGGG	CTGGGCGAGTTCAACAGCTCTATACGGGACCGGGGCTCTGTGAGAGGACGCG	480	
Db	421	AGTGGGGG	CTGGGCGAGTTCAACAGCTCTATACGGGGACCGGGGCTCTGTGAGAGGACGCG	480	
QY	481	CGTCTGC	GGGAGGGGAACTGGGCATCACTGATGAGGCAAGTCTGACGGGGGCGCTGTGGCACTG	540	
Db	481	CGTCTGC	GGGAGGGGAACTGGGCATCACTGATGAGGCAAGTCTGACGGGGGCGCTGTGGCACTG	540	
QY	541	GGGGCCCT	GTGTAATCTGTAGGGGCTTTTGTGCTAGCAAGTG	581	
Db	541	GGGGCCCT	GTGTAATCTGTAGGGGCTTTTGTGCTAGCAAGTG	581	

RESULT 4							
LOCUS	AY185100	1110 bp	mRNA	linear	ROD 24-JUN-2003		
DEFINITION	Rattus norvegicus BCL-WEL mRNA, complete cds.						
ACCESSION	AY185100						
VERSION	AY185100.1	GI:32185284					
KEYWORDS							
SOURCE							
ORGANISM	Rattus norvegicus (Norway rat)						
	Rattus norvegicus						
	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;						
	Rattus.						
	1 (bases 1 to 1110)						
REFERENCE	Itoh T., Itoh A. and pleasure D.						
AUTHORS	Bcl-2-related protein family gene expression during						
TITLE	oligodendroglial differentiation						
JOURNAL	J. Neurochem. 85 (6), 1500-1512 (2003)						
MEDLINE	22672518						

PUBMED 12787069
REFERENCE 2 (bases 1 to 1110)
AUTHORS Itch, T., Itch, A. and Pleasure, D.
TITLE Direct Submission
JOURNAL Submitted (21-Nov-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA

FEATURES
SOURCE
1. 1110
/organism="Rattus norvegicus"
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/strain="Sprague-Dawley"
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K"

CDS

1 ATGGGACCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 60
509 ATGGGAGCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 568
61 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 120
569 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 628
121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180
629 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 688
181 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
689 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 748
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749 CAGGTTTCCGAGCAATTTTCCAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTT 808
301 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 360
809 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 868
361 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 420
869 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 928
421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 480
929 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 988
481 CCTTCGCGGAGAGGAGACGCGGACATGAGAGAGACGCTGACGCGGGCGCTGGGACAG 540
989 CCTTCGCGGAGAGGAGACGCGGACATGAGAGAGACGCTGACGCGGGCGCTGGGACAG 1048
541 GGGGCGCTGTGTAAGTGTAGGCGCTTTTGTGCTAGCAAGTG 581
1049 GGGGCGCTGTGTAAGTGTAGGCGCTTTTGTGCTAGCAAGTG 1089

ORIGIN

Query Match 97.2%; Score 565; DB 10; Length 1110;
Best Local Similarity 98.3%; Pred. No. 3.9e-127;
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 ATGGGACCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 60
509 ATGGGAGCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 568
61 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 120
569 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 628
121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180
629 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 688
181 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
689 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 748
241 CAGGTTTCCGAGCAATTTTCCAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTT 300
749 CAGGTTTCCGAGCAATTTTCCAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTT 808
301 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 360
809 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 868
361 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 420
869 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 928
421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 480
929 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 988
481 CCTTCGCGGAGAGGAGACGCGGACATGAGAGAGACGCTGACGCGGGCGCTGGGACAG 540
989 CCTTCGCGGAGAGGAGACGCGGACATGAGAGAGACGCTGACGCGGGCGCTGGGACAG 1048
541 GGGGCGCTGTGTAAGTGTAGGCGCTTTTGTGCTAGCAAGTG 581
1049 GGGGCGCTGTGTAAGTGTAGGCGCTTTTGTGCTAGCAAGTG 1089

RESULT 5
AY185098
LOCUS

AY185098 3487 bp mRNA linear ROD 24-JUN-2003

DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION AY185098
VERSION AY185098.1 GI:32185280
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 3487)

AUTHORS Itch, T., Itch, A. and Pleasure, D.

TITLE Bcl-2-related protein family gene expression during

JOURNAL oligodendroglial differentiation

MEDLINE J. Neurochem. 85 (6), 1500-1512 (2003)

2672518

12787069

2 (bases 1 to 3487)

AUTHORS Itch, T., Itch, A. and Pleasure, D.

TITLE Direct Submission
JOURNAL Submitted (21-Nov-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA

Location/Qualifiers

FEATURES

source

1. 3487
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/product="BCL-W"
/protein_id="AA064468.1"
/db_xref="GI:32185281"

CDS

1 ATGGGACCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 60
170 ATGGGAGCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 229
61 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 120
230 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 289
121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180
290 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 349
181 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
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470 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 529
361 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 420
530 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 589
421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 480

ORIGIN

Query Match 97.2%; Score 565; DB 10; Length 3487;
Best Local Similarity 98.3%; Pred. No. 3.4e-127;
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 ATGGGACCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 60
170 ATGGGAGCCCAAGCTCAACCCAGACACACAGGGCTAGTGGCTGACTTTGTAGGCTAT 229
61 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 120
230 AAGCTGAGCAAGAGGTTATGCTGTGAGCTGCGCCCTGGGGAAGGCCACCCGAC 289
121 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 180
290 CCGCTGACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTCCGCGCAC 349
181 TTCTCTGACCTGCGCTCAGCTACACGTAACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
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241 CAGGTTTCCGAGCAATTTTCCAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTT 300
410 CAGGTTTCCGAGCAATTTTCCAGGGGCGCTTAAGTGGGCGCTTGTGGCATTCTT 469
301 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 360
470 GTCTTTGGGGGCGCTGCTGAGTGTGACGAGTGTCAAGAAATGAGCCTTGTGGGGA 529
361 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 420
530 CAGTGCAGAGATTGATGTGCTGCTACCTGAGACACGCTGTGCTGATGATCCACAGC 589
421 AGTGGGGGCTGGGCGGAGTTCAAGCTCTATACGCGGAGCGGGCGCTTGGAGAGGACG 480

Db 590 AGTGGGGCTGGGGGAGTTCACTCTATACCGGGACCGGGCCCTGGAGAGGCAACG 649

Qy 481 CGTCTGAGGAGGAGGAACTGGGGCATCATGTGAGGACAGTGTGACGGGGCCCTGGCACTG 540

Db 650 CGTGTGGGAGGAGGAACTGGGGCATCATGTGAGGACAGTGTGACGGGGCCCTGGCACTG 709

Qy 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGT 581

Db 710 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGT 750

RESULT 6
AY170344 3473 bp mRNA linear ROD 22-SEP-2003
LOCUS Mus musculus Bcl2-like protein 2 mRNA, complete cds.
DEFINITION AY170344
ACCESSION AY170344.2 GI:34857712
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3473)
AUTHORS Su,H.-Y.
TITLE Extraction from neonatal mouse skin after IGF-1 stimulation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3473)
AUTHORS Su,H.-Y.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1, Heueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
3 (bases 1 to 3473)
AUTHORS Su,H.-Y.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1, Heueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
Sequence update by submitter
On Sep 22, 2003 this sequence version replaced gi:27497698.
REMARK
JOURNAL
FEATURES
COMMENT
SOURCE
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ORIGIN
Query Match 96.7%; Score 561.8; DB 10; Length 3473;
Best Local Similarity 97.9%; Pred. No. 2.1e-126; Indels 0; Gaps 0;
Matches 569; Conservative 0; Mismatches 12;

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Qy 1 ATGGGAGCCCAAGCTCAACCCAGACACACGAGGCTCTAGTGTGACTTTGTAGGCTAT 60

Db 182 ATGGGAGCCCAAGCTCAACCCAGACACACGAGGCTCTAGTGTGACTTTGTAGGCTAT 241

Qy 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAAAGCCGACCGGAC 120

Db 242 CAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAAAGCCGACCGGAC 301

Qy 121 CCGCTGACCAAGCATGCGGGCTGTGGAGACGAGTTTGACCCGTTTCCGCGGAC 180

Db 302 CCGCTGACCAAGCATGCGGGCTGTGGAGACGAGTTTGACAGACCCGTTTCCGCGGAC 361

Qy 181 TTCTTACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAAGCTTCAAC 240

Db 362 TTCTTACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAAGCTTCAAC 421

Qy 241 CAGGTTTCCAGCAAGATTTTCCAGAGGGGCTTAAGTGGGCGCTCTTGTGGCAATCTTT 300

Db 422 CAGGTTTCCAGCAAGATTTTCCAGAGGGGCTTAAGTGGGCGCTCTTGTGGCAATCTTT 481

Qy 301 GTCTTTGGGGCTGCTCTGTGTCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 360

Db 482 GTCTTTGGGGCTGCTCTGTGTCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 541

Qy 361 CAGTGAGAGATTGAGTGTGGCTTACCTTGGAGACAGTCTGGCTGAGTGGATCAAGC 420

Db 542 CAGTGAGAGATTGAGTGTGGCTTACCTTGGAGACAGTCTGGCTGAGTGGATCAAGC 601

Qy 421 AGTGGGGCTGGGGGAGTTCAACAGTCTATACGGGACCGGGCCCTGGAGAGGCAACG 480

Db 602 AGTGGGGCTGGGGGAGTTCAACAGTCTATACGGGACCGGGCCCTGGAGAGGCAACG 661

Qy 481 CGTCTGCGGAGAGGGAATCGGGCATCATGTGAGACAGTGTCTGACGGGGCCCTGGCACTG 540

Db 662 CGTCTGCGGAGAGGGAATCGGGCATCATGTGAGACAGTGTCTGACGGGGCCCTGGCACTG 721

Qy 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGT 581

Db 722 GGGGCCCTGGTAACTGTAGGGGCTTTTGTGCTAGCAAGT 762

RESULT 7
AR020779 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020779
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 1 04-AUG-1998;
FEATURES
SOURCE location/Qualifiers
1. .579
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ORIGIN
Query Match 96.6%; Score 561.4; DB 6; Length 579;
Best Local Similarity 98.1%; Pred. No. 3.2e-126;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 181 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAAAGCCGACCGGAC 120

Qy 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAAAGCCGACCGGAC 120

Db 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAAAGCCGACCGGAC 120

Qy 121 CCGCTGACCAAGCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTTCCGCGGAC 180

Db 121 CCGCTGACCAAGCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTTCCGCGGAC 180

Qy 181 TTCTTGAACCTGGCCGCTCAGCTACAGTACACCCAGGCTTACGCCAGCAAGCTTCAAC 240

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Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAG 579
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAG 579

RESULT 8
AX022531 581 bp DNA linear PAT 07-SEP-2000
LOCUS AX022531
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.

REFERENCE
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
location/Qualifiers
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RLRGNMA"

ORIGIN
Query Match 96.4%; Score 560.2; DB 6; Length 581;
Best Local Similarity 97.8%; Pred. No. 6.2e-126;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTCAACCCAGACACAGGGGCTGTGAGTGAATCTTTAGAGCTAT 60
Db 1 ATGGGACCCCAAGCTCAACCCAGACACAGGGGCTGTGAGTGAATCTTTAGAGCTAT 60
Qy 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGTGTGGCCCTGGGAAAGGCCAGCCGCGAC 120
Db 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGTGTGGCCCTGGGAAAGGCCAGCCGCGAC 120
Qy 121 CGGCTGCACCAAGCCATGCGGGCTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
Db 121 CGGCTGCACCAAGCCATGCGGGCTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
Qy 181 TTCTGTGACCTGGCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAAGCTTCAAC 240

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Qy 301 GCTTTGGGGGCTGCCCTGTGCTGAGTGTCAAGTAACAAGAAATGAGCCCTTGTGGGA 360
Db 301 GCTTTGGGGGCTGCCCTGTGCTGAGTGTCAAGTAACAAGAAATGAGCCCTTGTGGGA 360
Qy 361 CAAGTGCAGGATTTGATGTGCTGACCTGAGAGACAGTGTGCTGACTGTATCCACAGC 420
Db 361 CAAGTGCAGGATTTGATGTGCTGACCTGAGAGACACCTGTGCTGACTGTATCCACAGC 420
Qy 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCAGC 480
Db 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCAGC 480
Qy 481 CGTGTGGGGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGGCGTGGCACTG 540
Db 481 CGTGTGGGGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGGCGTGGCACTG 540
Qy 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 9
AX030819 581 bp DNA linear PAT 20-SEP-2000
LOCUS AX030819
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.

REFERENCE
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
location/Qualifiers
source 1..581
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RLRGNMA"

ORIGIN
Query Match 96.4%; Score 560.2; DB 6; Length 581;
Best Local Similarity 97.8%; Pred. No. 6.2e-126;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTCAACCCAGACACAGGGGCTGTGAGTGAATCTTTAGAGCTAT 60
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Query Match 90.6%; Score 526.6; DB 9; Length 582;
 Best Local Similarity 94.1%; Pred. No. 9.7e-118;
 Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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RESULT 12
LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2001
DEFINITION Human mRNA for KIAA0271 gene, complete cds.
ACCESSION D87461.1 GI:1944417
VERSION KIAA0271.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,
AUTHORS Chara,O., Tanaka,A., Kocani,H., Miyajima,N. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain
JOURNAL DNA Res. 3 (5), 321-329 (1996)
MEDLINE 97191544
PUBMED 9039502
REFERENCE 2 (bases 1 to 3542)
AUTHORS Chara,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1996) Osamu Chara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan

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FEATURES

source

(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

Location/Qualifiers

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ORIGIN

Query Match 90.1%; Score 523.4; DB 9; Length 3542;
 Best Local Similarity 93.8%; Pred. No. 4.7e-117;
 Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: EP 0932674-A 6 04-AUG-1999;
JOURNAL AMRAD OPERATIONS PTY LTD (AU)
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ORIGIN
Query Match 89.8%; Score 521.8; DB 6; Length 583;
Best Local Similarity 93.6%; Pred. No. 1.4e-116;
Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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DB 541 GGGGCGCTGGTAAGTGAAGGGCCCTTTTCTGTAACAAGT 581
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DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE unidentified
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REFERENCE
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
JOURNAL ADAMS JERRY MCKEE (AU); HOLMGREN SHAUN P (AU); CORY SUZANNE (AU)
; GIBSON LEONIE W (AU); AMRAD OPERATIONS PTY LTD (AU)
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ORIGIN
Query Match 89.8%; Score 521.8; DB 6; Length 583;
Best Local Similarity 93.6%; Pred. No. 1.4e-116;
Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGGCTCAACCCAGACACAGGGGCTCTAGTGTGAGGCTAT 60
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 14:27:07 ; Search time 397 Seconds

(without alignments)
6217.136 Million cell updates/sec

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Scoring table: IDENTITY NUC
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Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	565	97.2	582	9	ADB5296 Primary r
3	561.4	96.6	579	2	AAV28333 Rat bcl-y
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ALIGNMENTS

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DT 05-JUL-1999 (first entry)
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KW animal model; ss.
XX OS
XX Mus sp.
XX PN
XX WO9913710-A1.
XX PD
XX 25-MAR-1999.
XX PF
XX 16-SEP-1998; 98WO-AU000764.
XX PR
XX 16-SEP-1997; 97AU-00009228.
XX PA
XX (HALL-) HALL INST MEDICAL RES WALTER & ELITA.
XX PI
XX Cory S, Adams J, Print C, Gibson L, Koentgen F,
XX WPI; 1999-243890/20.
XX P-PSDB; AAY05531.
XX PT
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX PS
XX Claim 3; Page 34; 52pp; English.
XX CC
XX The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
XX AA05531), a pro-survival member of the Bcl-2 family which is widely
XX expressed and which is essential for spermatogenesis. The invention
XX relates generally to a method of treatment and to an animal model for
XX identification of molecules and genetic sequences useful for inducing or
XX reducing fertility of male animals. Methods are provided for the
XX treatment of infertility, or for reducing fertility, by modulating
XX spermatogenesis. An animal model carries a mutation is at least one
XX allele of the human or murine bcl-w gene or in a gene associated with bcl
XX -w. Such animals have disorganised seminiferous tubules and are
XX substantially infertile, but possess no other major abnormalities as

CC determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 581; DB 2; Length 581;
 Best Local Similarity 100.0%; Pred. No. 6,5e-146;
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC ADB52996;
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DT 04-DEC-2003 (first entry)
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XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; ds.
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
XX
PD 14-AUG-2003.
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PF 04-FEB-2003; 2003WO-US003482.
  
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XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
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PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
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XX (GENE-) GENE LOGIC INC.
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
DR WPI, 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of tox mean and non-tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3538; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the tox mean and non-tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 97.2%; Score 565; DB 9; Length 582;
Best Local Similarity 98.3%; Pred. No. 1.3e-141;
Matches 571; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTTCAACCCAGACACACGCGGCTTATGAGTGAATTTGAGCTTAT 60
DB 1 ATGGGACCCCAAGCTTCAACCCAGACACACGCGGCTTATGAGTGAATTTGAGCTTAT 60
QY 61 AAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 AAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGAGAGTTTGAAGACCGTTTCCGCGCACC 180
DB 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGAGAGAGTTTGAAGACCGTTTCCGCGCACC 180
QY 181 TTCTGTGACCTGCGCGCTCAGCTACACGTGACCCGAGCTCAGCCAGCAAGCTTACCC 240
DB 181 TTCTGTGACCTGCGCGCTCAGCTACACGTGACCCGAGCTCAGCCAGCAAGCTTACCC 240
QY 241 CAGGTTTCCGAGCAACTTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
  
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Db      241 CAGGTTCCGACGAACTTTCCAGAGGGGCCCCCACTGGGGCCGCTTGTGGCAATTCCTT 300
Qy      301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
Db      301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
Qy      361 CAAGTGCAGATTGGATGTGGCTTACCTGTGAGACAGCTGTGCTGACTGTGATCCACAGC 420
Db      361 CAAGTGCAGATTGGATGTGGCTTACCTGTGAGACAGCTGTGCTGACTGTGATCCACAGC 420
Qy      421 AGTGGGGCTTGGGCGAGATTCAAGCTTATACGGGGACGGGGCCCTGGAGAGGCAAGC 480
Db      421 AGTGGGGCTTGGGCGAGATTCAAGCTTATACGGGGACGGGGCCCTGGAGAGGCAAGC 480
Qy      481 CGTCTGCGGGAGGGGAACTGGGCACTGAGAGACAGTGTGAGACGGGGGCGTGGCACTG 540
Db      481 CGTCTGCGGGAGGGGAACTGGGCACTGAGAGACAGTGTGAGACGGGGGCGTGGCACTG 540
Qy      541 GGGGCCCTGTGAAGTGTAGAGGGGCTTTTGTGCTAGCAAGTG 581
Db      541 GGGGCCCTGTGAAGTGTAGAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 3
AAV28333
ID      AAV28333 standard; cDNA, 579 BP.
AC      AAV28333;
AAV28333;
DT      02-OCT-1998 (first entry)
XX      Rat bcl-y gene.
XX      66; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX      Rattus sp.
XX      Location/Qualifiers
FH      Key 1..579
FT      CDS /*tag= a
FT      /product= "bcl-y"
FT      /note= "No stop codon given"
XX      US5789201-A.
XX      04-AUG-1998.
XX      11-FEB-1997; 97US-00798897.
XX      23-FEB-1996; 96US-0012201P.
XX      (COCE-) COCENSYS INC.
XX      Guastella J;
XX      WPI; 1998-446079/38.
XX      P-PSDB; AAW61391.
XX      Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX      recombinant protein for use in treating uncontrolled cell growth e.g.
XX      cancers.
XX      Claim 2; Column 13/14; 27p; English.
XX      The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX      family, components in the cell death pathway. The bcl-2 family have both
XX      apoptotic activity and the apoptosis blocking activity. bcl-y falls in
XX      the apoptosis activity category. The recombinant protein may be used to
XX      prevent uncontrolled cell growth, either by its direct administration to
XX      recombinant genetic constructs to increase its expression in vivo. Also,
XX      antisense constructs can be used in disorders where prevention of cell
XX      death is desired
XX
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SQ      Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 1.2e-140;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy      1 ATGGCAGACCCAGGCTCAACCCAGACACACAGGGCTCTAGTGTGCTGACTTTGTAGAGCTAT 60
Db      1 ATGGCAGACCCAGGCTCAACCCAGACACACAGGGCTCTAGTGTGCTGACTTTGTAGAGCTAT 60
Qy      61 AAGCTGAGAGCAAGAGGTTATGTGTGTGAGAGCTGGCCCTTGGAGAGGCCAGCCGCGAC 120
Db      61 AAGCTGAGAGCAAGAGGTTATGTGTGTGAGAGCTGGCCCTTGGAGAGGCCAGCCGCGAC 120
Qy      121 CCGCTGACCAACCAAGCATGGGGCTGTGTGAGAGACAGATTTGAGACCCGTTTCCGCGGAC 180
Db      121 CCGCTGACCAACCAAGCATGGGGCTGTGTGAGAGACAGATTTGAGACCCGTTTCCGCGGAC 180
Qy      181 TTCTCTGACCTGGGCGGCTCAAGCTACAGTGAACCCAGGCTCAGGCCAGCAAGCTTGAC 240
Db      181 TTCTCTGACCTGGGCGGCTCAAGCTACAGTGAACCCAGGCTCAGGCCAGCAAGCTTGAC 240
Qy      241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCAATTCCTT 300
Db      241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGTGGCAATTCCTT 300
Qy      301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
Db      301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
Qy      361 CAAGTGCAGATTGGATGTGGCTTACCTGTGAGACAGCTGTGCTGACTGTGATCCACAGC 420
Db      361 CAAGTGCAGATTGGATGTGGCTTACCTGTGAGACAGCTGTGCTGACTGTGATCCACAGC 420
Qy      421 AGTGGGGCTTGGGCGAGATTCAAGCTTATACGGGGACGGGGCCCTGGAGAGGCAAGC 480
Db      421 AGTGGGGCTTGGGCGAGATTCAAGCTTATACGGGGACGGGGCCCTGGAGAGGCAAGC 480
Qy      481 CGTCTGCGGGAGGGGAACTGGGCACTGAGAGACAGTGTGAGACGGGGGCGTGGCACTG 540
Db      481 CGTCTGCGGGAGGGGAACTGGGCACTGAGAGACAGTGTGAGACGGGGGCGTGGCACTG 540
Qy      541 GGGGCCCTGTGAAGTGTAGAGGGGCTTTTGTGCTAGCAAG 579
Db      541 GGGGCCCTGTGAAGTGTAGAGGGGCTTTTGTGCTAGCAAG 579

RESULT 4
AAI15945
ID      AAI15945 standard; cDNA, 579 BP.
AC      AAI15945;
AAI15945;
DT      20-MAY-1999 (first entry)
XX      cDNA encoding the rat bcl-y protein.
XX      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX      programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX      head trauma; Alzheimer's disease; neural; muscular degenerative disease;
XX      multiple sclerosis; myocardial infarction; vitally induced cell death;
XX      aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX      premature cell death; cell death stimulator; prolonged cell life span;
XX      Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
XX      ss.
XX      Rattus sp.
XX      US5883229-A.
XX      16-MAR-1999.
XX      25-NOV-1997; 97US-00978523.
XX
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XX 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI: 1999-214150/18.
XX P-PSDB; AAW97391.
DR
XX
XX Novel bcl-1 homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX
XX Disclosure; Col 13-16; 26pp; English.
XX
XX The present sequence encodes rat bcl-1 protein (Rbcl-1). The
XX specification also describes human bcl-1 protein (Hbcl-1). Rbcl-1 and
XX Hbcl-1 are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-1 and Hbcl-1
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-1 and
XX Hbcl-1 may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites
XX
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 1.2e-140;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCCAAGCCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AAGCTGAGCAGAAAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGCGAC 120
DB 61 AAGCTGAGCAGAAAGGCTTATGCTGTGAGCTGCGCTTGGGAGAGCCAGCCGCGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGACGAGTTTGAAGCCCGTTTCCGCGCACC 180
DB 121 CCGCTGACCAAGCCATGCGGGGCTGTGAGACGAGTTTGAAGCCCGTTTCCGCGCACC 180
QY 181 TTCTCGACCTGCGCGCTCAGCTACACGTGACCCAGGCTCAAGCCAGCAAGCTTACCC 240
DB 181 TTCTCGACCTGCGCGCTCAGCTACACGTGACCCAGGCTCAAGCCAGCAAGCTTACCC 240
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGCGGCGCTTTGTGGCATTTCTT 300
DB 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCTTACTGCGGCGCTTTGTGGCATTTCTT 300
QY 301 GTCCTTGGGGGCGCGCTGTGTGCTGAGAGTTCAAAGAAATGAGGCTTTGGTGGGA 360
DB 301 GTCCTTGGGGGCGCGCTGTGTGCTGAGAGTTCAAAGAAATGAGGCTTTGGTGGGA 360
QY 361 CAAGTCAGAGATTTGATGCTGCTGAGACACGCTGTGGCTGACTGATCCACAGC 420
DB 361 CAAGTCAGAGATTTGATGCTGCTGAGACACGCTGTGGCTGACTGATCCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGAGGAGCGGGCGCTTGAAGAGGACGG 480
DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGAGGAGCGGGCGCTTGAAGAGGACGG 480
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QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCACTAGAGACAGTGTCTGACGGGGCGCTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGGAACTGGGCATCACTAGAGACAGTGTCTGACGGGGCGCTGGCACTG 540
QY 541 GGGGCGCTGTTAATCTGTAGGGGCGCTTTTGTCTAGCAAG 579
DB 541 GGGGCGCTGTTAATCTGTAGGGGCGCTTTTGTCTAGCAAG 579
RESULT 5
AAT96578
ID AAT96578 standard; DNA; 581 BP.
AC AAT96578;
XX
XX 22-APR-1998 (first entry)
XX
XX Mouse bcl-w DNA.
XX
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..507
XX FT /tag= a
XX FT /product= "bcl-w"
XX FT /note= "q"
XX
XX WO9735971-A1.
XX
XX 02-OCT-1997.
XX
XX 27-MAR-1997; 97WO-AU000199.
XX
XX 27-MAR-1996; 96AU-00008965.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
XX MPI: 1997-489635/45.
XX
XX P-PSDB; AAW36048.
XX
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX inhibit cell survival, e.g. for treatment of cancer and degenerative
XX diseases.
XX
XX PS Claim 3; Page 50-51; 86pp; English.
XX
XX This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
XX family. This gene promotes cell survival, so its modulation is useful in
XX treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
XX stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
XX hypoxia, ischaemia, human immunodeficiency virus infection or in cell
XX transplants. Up-regulation of the gene can also be used to modify cell
XX lines cultured in vivo, e.g. to develop new lines, to facilitate
XX isolation of hybridomas and to increase survival of primary explants
XX during genetic modification. It can be used to produce recombinant Bcl-w
XX for therapy, diagnosis, antibody production or screening of potential
XX modulators
XX
XX
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;
Query Match 96.4%; Score 560.2; DB 2; Length 581;
Best Local Similarity 97.8%; Pred. No. 2.5e-140;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCCAAGCCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
```

QY	61	AAGCTGAGAGGACAGAGGGTATATGTCGTGGAGAGCTGGGCGCTGGGGAAAGGCCAGCGCGGAC	120
Db	61	AGGCTGAGAGGACAGAGGGTATATGTCGTGGAGAGCTGGGCGCTGGGGAAAGGCCAGCGCGGAC	120
QY	121	CCGCTGCACCAAGCCATGCGGGGCTGCTGGAGACGAATTTTGAGACCCGGTTCGCGCGACC	180
Db	121	CCGCTGCACCAAGCCATGCGGGGCTGCTGGAGAGCAATTTTGAGACCCGGTTCGCGCGACC	180
QY	181	TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAAGGCTCAAGCCAGCAAGCCTTCACC	240
Db	181	TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAAGGCTCAGCCAGCAAGCCTTCACC	240
QY	241	CAGGTTTCCGACGAATCTTTCCAAAGGGGGCCCTTAATCTGGGGCGCTTGTGTGACATCTTT	300
Db	241	CAGGTTTCCGACGAATCTTTCCAAAGGGGGCCCTTAATCTGGGGCGCTTGTGTGACATCTTT	300
QY	301	GTCCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGTGGGA	360
Db	301	GTCCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGTGGGA	360
QY	361	CAAGTGCAGAGATTGGATGATGTGGCCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC	420
Db	361	CAAGTGCAGAGATTGGATGATGTGGCCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC	420
QY	421	AGTGGGGGCTGGGCGGAGTTCAACAGCTCTAATACGGGGACGGGGCCCTGGAGAGGCAAGG	480
Db	421	AGTGGCGGGCTGGGCGGAGTTCAACAGCTCTAATACGGGGACGGGGCCCTGGAGAGGCAAGG	480
QY	481	CGTCCTGGGGAGGGGAACTGGGCATAGTGAAGGACAGTGTGACGGGGGCGTGGGCACTG	540
Db	481	CGTCCTGGGGAGGGGAACTGGGCATAGTGAAGGACAGTGTGACGGGGGCGTGGGCACTG	540
QY	541	GGGGCCCTGGTAACTGTAGAGGGGCTTTTTCCTAGCAAGTG	581
Db	541	GGGGCCCTGGTAACTGTAGAGGGGCTTTTTCCTAGCAAGTG	581

RESULT	6	
AAK25135		
ID	AAK25135	standard; DNA; 581 BP.
XX		
XX	AAK25135;	
AC		
DT	05-JUL-1999	(first entry)
XX		
DE	Mouse bcl-w gene derivative.	
XX		
KW	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;	
KM	animal model; ss.	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..507
FT		/*tag= a
XX		
PN	W09913710-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998;	98MO-AU000764.
XX		
PR	16-SEP-1997;	97AU-00009228.
XX		
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
XX		
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F;	
XX		
DR	WPI; 1999-243890/20.	
XX		
DR	P-PSDB; AAY05533.	
XX		
FT	An animal model exhibiting reduced levels of a Bcl-w protein and/or	
FT	protein associated with Bcl-w.	

XX
PS Disclosure; Page 38; 52pp; English.

CC The present sequence is described as a derivative of the mouse bcl-w gene
CC (see AAX25133) and encodes Bcl-w protein (see AAY05533), a pro-survival
CC member of the Bcl-2 family which is widely expressed and which is
CC essential for spermatogenesis. The invention relates generally to a
CC method of treatment and to an animal model for the identification of
CC molecules and genetic sequences useful for inducing or reducing fertility
CC of male animals. Methods are provided for the treatment of infertility,
CC or for reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation in at least one allele of the human or murine bcl-w
CC gene or in a gene associated with bcl-w. Such animals have disorganised
CC seminiferous tubules and are substantially infertile, but possess no other
CC major abnormalities as determined by histological examination. They can
CC be used to screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis
CC in animals, or which can induce infertility

SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match	96.4%	Score 560.2;	DB 2;	length 581;
Best Local Similarity	97.8%	Pred. No. 2.5e-140;		
Matches 568; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

QY	1	ATGCGACACCCAGCCTCAACCCCAAGACAACGGGCTCTAGTGGCTGACCTTTTAAAGCTAT	60
Db	1	ATGCGACACCCAGCCTCAACCCCAAGACAACCGGCTCTAGTGGCTGACCTTTTAAAGCTAT	60
QY	61	AAGCTGAGGACGAAGAAGGTTATGTCTGTGAGAGCTGACCCTGGGGGAAGGCCACCGCGAC	120
Db	61	AAGCTGAGGACGAAGAAGGTTATGTCTGTGAGAGCTGAGGCTGGGGGAAGGCCACCGCGAC	120
QY	121	CCGCTGCACCAAGCCATCGGGCTGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCAC	180
Db	121	CCGCTGCACCAAGCCATCGGGCTGCTGTGAGACGAGTTTGAGAACCCGTTTCCGCGCAC	180
QY	181	TTTCTGTACCTTGGCCGCTCAGCTACACGTGAACCCAGGCTCAGGCCAAGAACGTTCAAC	240
Db	181	TTTCTGTACCTTGGCCGCTCAGCTACACGTGAACCCAGGCTCAGGCCAAGAACGTTCAAC	240
QY	241	CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAACCTGGGGCGCTTGTGTGACATCTTT	300
Db	241	CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTTAACCTGGGGCGCTTGTGTGACATCTTT	300
QY	301	GTCTTTGGGGGTGCCCTGTGTGTCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA	360
Db	301	GTCTTTGGGGGTGCCCTGTGTGTCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA	360
QY	361	CAAGTGCAGAAATTGGATGTGTGGCTTAACCTGGAGACACGTCTGTGCTGACTGTGAATCCACAGC	420
Db	361	CAAGTGCAGAAATTGGATGTGTGGCTTAACCTGGAGACACGTCTGTGCTGACTGTGAATCCACAGC	420
QY	421	AGTGGGGGCTGGGGGGAGTTCAACAGCTCTAATCGGGGACGGGGCCCTGGAGGAGGCACGG	480
Db	421	AGTGGGGGCTGGGGGGAGTTCAACAGCTCTAATCGGGGAGCGGGGCCCTGGAGGAGGCACGG	480
QY	481	CGTCTGCAGGAGGGGACCTGGGCATCACTGAGAGACAGTGTCTGACGGGGGCGTGTGCACTG	540
Db	481	CGTCTGCAGGAGGGGACCTGGGCATCACTGAGAGACAGTGTGTACGGGGGCGTGTGCACTG	540
QY	541	GGGGCCCTGTGTACTGTAGGGGCGCTTTTGTGTAGCAAGTG	581
Db	541	GGGGCCCTGTGTACTGTAGGGGCGCTTTTGTGTAGCAAGTG	581

RESULT 7	
ABV78153	
ID	ABV78153 standard; DNA; 582 BP
AC	
XX	
XX	ABV78153;
XX	
DT	15-NOV-2002 (first entry)

XX Human bcl-w DNA SEQ ID NO 37.
 DE RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cyrostatic;
 KM virucide; protozoacide; gene; ds.
 KM Homo sapiens.
 OS WO200255693-A2.
 PN 18-JUL-2002.
 XX 09-JAN-2002; 2002WO-EP000152.
 PF 09-JAN-2001; 2001DE-01000586.
 PR 26-OCT-2001; 2001DE-01055280.
 PR 29-NOV-2001; 2001DE-01058411.
 PR 07-DEC-2001; 2001DE-01060151.
 XX (RIBO-) RIBOPHARMA AG.
 PA Kreutzer R, Limmer S, Rost S, Hadwiger P;
 PI WPI; 2002-590671/63.
 DR Inhibiting expression of target gene, useful e.g. for inhibiting
 PT oncogenes, by administering double-stranded RNA complementary to the
 PT target and having an overhang.
 XX Claim 10; Page 134; 203pp; German.
 XX The invention relates to inhibiting expression of a target gene (I) in a
 CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
 CC structure of at most 49 consecutive bases. At least part of one strand
 CC (as1) of dsRNA1 is complementary to (i) and at least one end of dsRNA1
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
 CC in humans, also genes in plasmodium or in viruses or viroids that are
 CC pathogenic for humans, animals or plants. Introducing an overhang into
 CC dsRNA greatly increases effectiveness for inhibiting gene expression,
 CC both in vivo and in vitro and also increases stability and thus the
 CC effective concentration inside the cell. The present sequence is that of
 CC a gene related to the invention
 XX
 XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
 SQ
 Query Match 90.6%; Score 526.6; DB 6; Length 582;
 Best Local Similarity 94.1%; Pred. No. 2.6e-131;
 Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 361 CAAGTCAGAGATTGGATGGTGGCTTACCTGAGACACAGCTGTGGTGAAGTGCACAGC 420
 DB 361 CAAGTCAGAGATTGGATGGTGGCTTACCTGAGACAGCGGCTGGCTGATGCACAGC 420
 QY 421 AGTGGGCGCTGGCGGAGCTTATACAGCTTATACCGGAGCGGGCCCTGGAGAGGACAGG 480
 DB 421 AGTGGGCGCTGGCGGAGCTTATACAGCTTATACCGGAGCGGGCCCTGGAGAGGCGGCG 480
 QY 481 CGTCTGCGGAGGAGGAATGGGCAATCAGTGAAGGACAGTGCAGCGGGGCGGTGGCACTG 540
 DB 481 CGTCTGCGGAGGAGGAATGGGCAATCAGTGAAGGACAGTGCAGCGGGGCGGTGGCACTG 540
 QY 541 GGGGCCCTGTACTGTAGGGGCTTTTCTAGCAAGTG 581
 DB 541 GGGGCCCTGTACTGTAGGGGCTTTTCTAGCAAGTG 581
 RESULT 8
 AB235729
 ID AB235729 standard; DNA; 582 BP.
 XX AB235729;
 AC 07-FEB-2003 (first entry)
 DT Human bcl-w polynucleotide SEQ ID NO 37.
 DE Double stranded RNA; dsRNA; RNAi; RNA inhibition; cyrostatic; virucide;
 XX protozoacide; gene expression; antisense; tumor; infection; plasmodium;
 KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
 KW Hepatitis C virus; human papilloma virus; gene; ds.
 XX Homo sapiens.
 OS DE10100588-A1.
 XX 18-JUL-2002.
 PD 09-JAN-2001; 2001DE-01000588.
 PF 09-JAN-2001; 2001DE-01000588.
 PR 09-JAN-2001; 2001DE-01000588.
 XX (RIBO-) RIBOPHARMA AG.
 PA Kreutzer R, Limmer S, Rost S, Hadwiger P;
 PI WPI; 2002-683450/74.
 DR Inhibiting expression of target genes, useful e.g. for treating tumors,
 PT by introducing into cells two double-stranded RNAs that are complementary
 PT to the target.
 XX Claim 13; Page 30-31; 100pp; German.
 XX The invention relates to inhibiting expression of a target gene in a cell
 CC by introducing at least two oligonucleotides (dsRNA1 and II), both
 CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
 CC pairs. At least part of one strand (S1, S2) of the ds structures in each
 CC of dsRNA1 and II are complementary to regions in the target gene. The
 CC method uses antisense inhibition of gene expression using double stranded
 CC RNA inhibition (RNAi). The method is particularly used to treat tumours
 CC or infections, especially by plasmodium or viruses/viroids (pathogenic on
 CC humans, animals or plants). The method provides more effective inhibition
 CC of expression than known methods using a single dsRNA, even at very low
 CC concentrations. When dsRNA has at least one unpaired nucleotide at the
 CC end, stability (and thus effective concentration in the cell) is improved
 CC and efficiency can be increased further by pretreating the cells with
 CC interferon. The present sequence is that of a target DNA of the invention
 XX
 XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
 SQ
 Query Match 90.6%; Score 526.6; DB 6; Length 582;

Best Local Similarity 94.1%; Pred. No. 2.6e-131;
Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACAGGCGCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGGCGACCCAGCCTCGGCCAGACACACAGGCGCTGAGTGGAGACTTTGAGGCTAT 60
QY 61 AAGTGAAGGCAAGAGGTTATGTCTGGAGCTGGCCCGGAGAGGCGCCAGCGCTAC 120
DB 61 AAGTGAAGGCAAGAGGTTATGTCTGGAGCTGGCCCGGAGAGGCGCCAGCGCTAC 120
QY 121 CCGGTGACCAAGCATGCGGGCTGCTGAGACAGAGTTTGAAGCCGTTTCCGCGCAC 180
DB 121 CCGGTGACCAAGCATGCGGGCTGCTGAGACAGAGTTTGAAGCCGTTTCCGCGCAC 180
QY 181 TTCTGTGACTGGCGCTGAGCTGACAGTGAACCCAGGCTGAGCCCAAGCGCTTACC 240
DB 181 TTCTGTGACTGGCGGCTGAGCTGATGTAACCCAGGCTGAGCCCAAGCGCTTACC 240
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTTAAGGGGGCCGTTTGGCATTTCT 300
DB 241 CAGGTTCTCCGACGAACTTTTCCAAAGGGGGCCCAAGGGGGCCGTTTGTAGCCTTTCT 300
QY 301 GTCTTTGGGGCTGCGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 360
DB 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTGTGGGA 360
QY 361 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 CAAGTGCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 AGTGGGGGCTGGGGGAGTTCACAGCTTATACGGGGACGGGGCCCTGAGAGGAGCAG 480
DB 421 AGTGGGGGCTGGGGGAGTTCACAGCTTATACGGGGACGGGGCCCTGAGAGGAGCAG 480
QY 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581
DB 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581
```

RESULT 9
ABX09972
ID ABX09972 standard; DNA; 582 BP.

```
XX AC ABX09972;
XX DT 23-JAN-2003 (first entry)
XX DE Human bcl-w DNA fragment SEQ ID 37.
XX KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental.
XX KM prion; inhibition; human; ds.
XX OS Homo sapiens.
XX PN DE1010587-Cl.
XX PD 21-NOV-2002.
XX PF 09-JAN-2001; 2001DE-01000587.
XX PR 09-JAN-2001; 2001DE-01000587.
XX PA (RIBO-) RIBOPHARMA AG.
XX PI Kreutzer R, Limmer S, Roest S, Hadwiger P.
XX DR WPI; 2002-742209/81.
```

PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.

Disclosure; Page 35-36; 98pp; German.

This invention describes a novel method for inhibiting expression of a
target gene by introducing into the cell that contains the target gene at
least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
structure of not more than 49 consecutive nucleotides (nt), where at
least a segment of one strand of the ds structure is complementary with
the target gene and the cells are treated with interferon before
introduction of dsRNA. The method is used to inhibit expression of
target genes, particularly oncogenes, cytokine genes, Id (not defined)
protein genes, developmental or prion genes, or genes expressed in
pathogenic organisms (particularly plasmids) or in viruses or viroids
(pathogenic in humans, animals or plants). Treating the cells with
interferon greatly increases the extent to which dsRNA can inhibit
expression of the target genes, and the effect is even greater when dsRNA
are modified to increase their stability. ABX09936-ABX10075 represent
gene fragments used to illustrate the method of the invention

Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 90.6%; Score 526.6; DB 6; Length 582;
Best Local Similarity 94.1%; Pred. No. 2.6e-131;
Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACAGGCGCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGGCGACCCAGCCTCGGCCAGACACACAGGCGCTGAGTGGAGACTTTGAGGCTAT 60
QY 61 AAGTGAAGGCAAGAGGTTATGTCTGGAGCTGGCCCGGAGAGGCGCCAGCGCTAC 120
DB 61 AAGTGAAGGCAAGAGGTTATGTCTGGAGCTGGCCCGGAGAGGCGCCAGCGCTAC 120
QY 121 CCGGTGACCAAGCATGCGGGCTGCTGAGACAGAGTTTGAAGCCGTTTCCGCGCAC 180
DB 121 CCGGTGACCAAGCATGCGGGCTGCTGAGACAGAGTTTGAAGCCGTTTCCGCGCAC 180
QY 181 TTCTGTGACTGGCGCTGAGCTGACAGTGAACCCAGGCTGAGCCCAAGCGCTTACC 240
DB 181 TTCTGTGACTGGCGGCTGAGCTGATGTAACCCAGGCTGAGCCCAAGCGCTTACC 240
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTTAAGGGGGCCGTTTGGCATTTCT 300
DB 241 CAGGTTCTCCGACGAACTTTTCCAAAGGGGGCCCAAGGGGGCCGTTTGTAGCCTTTCT 300
QY 301 GTCTTTGGGGCTGCGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 360
DB 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTGTGGGA 360
QY 361 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 CAAGTGCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 AGTGGGGGCTGGGGGAGTTCACAGCTTATACGGGGACGGGGCCCTGAGAGGAGCAG 480
DB 421 AGTGGGGGCTGGGGGAGTTCACAGCTTATACGGGGACGGGGCCCTGAGAGGAGCAG 480
QY 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581
DB 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTCTAGCAAGTG 581
```

RESULT 10
ABL91694
ID ABL91694 standard; DNA; 582 BP.

AC	ABL91694;
XX	
DT	28-MAY-2002 (first entry)
DE	Human polynucleotide SEQ ID NO 37.
XX	
KM	Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW	Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
XX	Cytostatic; virucide; protozoacide; antibacterial; ds.
OS	Homo sapiens.
PN	DE10100586-C1.
XX	
PD	11-APR-2002.
PF	09-JAN-2001; 2001DE-01000586.
XX	
PR	09-JAN-2001; 2001DE-01000586.
PA	(RIBO-) RIBOPHARMA AG.
PI	Kreutzer R, Limmer S, Rost S, Hadwiger P,
XX	
DR	WPI; 2002-270454/32.
XX	
PT	Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT	introducing double-stranded complementary oligoRNA having unpaired
PT	terminal bases.
XX	
PS	Claim 13; Page 32; 104pp; German.
XX	
CC	The invention relates to a method for inhibiting expression of a target
CC	gene (ABL91695-ABL9197) in a cell by introducing at least one
CC	oligoribonucleotide that has a double-stranded structure consisting of at
CC	most 49 sequential nucleotide pairs, with at least part of one strand
CC	complementary with the target gene and has at least one end a single-
CC	stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC	antisense inhibition of gene expression useful e.g. for treating tumours
CC	but the oligoribonucleotides may also be directed against genes present
CC	in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
CC	animals or plants) or against cytokines, Id. developmental or prion genes.
CC	The method provides more effective inhibition of gene expression than use
CC	of known oligonucleotides, probably because the unpaired overhang
CC	increases stability and thus intracellular concentration
SQ	
	Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
Query Match	90.6%; Score 526.6; DB 6; Length 582;
Best Local Similarity	94.1%; Pred. No. 2.6e-131;
Matches 547; Conservative	0; Mismatches 34; Indels 0; Gaps 0
OY	1 ATGGGAGCCCCCGCCTCAACCCCAGACACAGCGGCCTGTAGTGGACTTTTGAGGCTAT 60
DB	1 ATGGGAGCCCCCGCCTCGGCCCAAGACACAGCGGCTCTGTGTGGACATTGTAGTTAT 60
OY	61 AAGCTGAGGACAGAAGGATTATGTCCTGTGAGGCTGGCCCTGGGAAAGGCCAGCCGCGAC 120
DB	61 AAGCTGAGGACAGAAGGATTATGTCGTGTGAGGCTGGCCCGGGGAAGGCCACAGCTGAC 120
OY	121 CGCTGACCAAGCCATGCGGGCTGTGTGAGACCAAGTTTGAACCCGCTTTCCGCGCAC 180
DB	121 CGCTGACCAAGCCATGCGGGCAGTGTGAAGTAGTTGACAACCCGCTTTCCGGGCAAC 180
OY	181 TTCTCTGACCTGGCGCGCTCAGCTAACAACGTAACCCAGGCTCAAGCCAGACGCTTACC 240
DB	181 TTCTCTGACCTGGCGCGCTCAGCTAACAACGTAACCCAGGCTCAAGCCAGACGCTTACC 240
OY	241 CAGGTTTTCCAGCACTTTTCCAAGGGGGCCCTTAACCTGGGCGCTTTGTGGCATTTCTT 300
DB	241 CAGGCTCCGAGCACTTTTCCAAGGGGGCCCACTGGGGCGCGCTTTGTAGCTTTCTT 300
OY	301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTCAACAAATAAGAACCTTTTGGTGGGA 360

Db	301	GTCTTTGGGGCTGCACCTGTCGTGTCGAGAGTGTCAACAAAGAGATGGAACTCACTGTTGGG	360
QY	361	CAAGTGCAGGATTGGATGTGTGGCTTAACCTGGAGACACGCTGGCTGATCTCCACAG	420
Db	361	CAAGTGCAGGAGTGAATGTGTGGCTTAACCTGGAGACGCGGCTGGCTGATCTGGATCCACAG	420
QY	421	AGTGGGGGCTGGGGCCGAGTTCAACAGCTCTAATGCGGGGACGGGGCCCTGGAGAGGCAAG	480
Db	421	AGTGGGGGCTGGGGCCGAGTTCAACAGCTCTAATGCGGGGACGGGGCCCTGGAGAGGCGCG	480
QY	481	CGTTCGCGGAGGCGGAACTGGGCATCAGTGAAGACAGTGTCTACGCGGGCCGTGGCACTG	540
Ddb	481	CGTTCGCGGAGGCGGAACTGGGCATCAGTGAAGACAGTGTCTGACGCGGGGCCGTGGCACTG	540
QY	541	GGGGCCCTGGTAACTGTAGAGGGGCCCTTTTTTGGTACCAAGTG	581
Ddb	541	GGGGCCCTGGTAACTGTAGAGGGGCCCTTTTTTGGTACCAAGTG	581

RESULT 11
 ID AAX25132 standard; DNA; 581 BP.
 AC AAX25132;
 DT 05-JUL-1999 (first entry)
 DE Human bcl-w gene.
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 OS Homo sapiens.
 PN W09913710-A1.
 PD 25-MAR-1999.
 PF 16-SEP-1998; 98MO-AU000764.
 PR 16-SEP-1997; 97AU-00009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
 DR WPI; 1999-243890/20.
 DR P-PSDB; AAY05530.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Claim 3; Page 32; 52pp; English.
 CC The present sequence is the human bcl-w gene encoding Bcl-w protein (see
 CC AAY05530), a pro-survival member of the Bcl-2 family which is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene or in a gene associated with bcl
 CC -w. Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities as
 CC determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

Query Match 90.1%; Score 523.4; DB 2; Length 581;
 Best Local Similarity 93.8%; Pred. No. 1.8e-130;
 Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
 DB 1 ATGGCGACCCCGCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGCCCGCCGAC 120
 DB 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGCGCCAGCAGCTTAC 120

QY 121 CCGCTGACCAAGCATGCGGCTGCTGAGACGAGTTTGAAGCCGTTCCGCGCAC 180
 DB 121 CCGCTGACCAAGCATGCGGCTGAGAGTGAAGTTGAGACCCGCTTCGCGCAC 180

QY 181 TTCTGTGACCTGGCGCTCAGCTACACGTGACCCGAGGCTCAGCCAGCAACGCTTCACC 240
 DB 181 TTCTGTGATCGGGGCTCAGCTGATGTGACCCGAGCTCAGCCAGCAACGCTTCACC 240

QY 241 CAGGTTTCCAGCAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTCTT 300
 DB 241 CAGGTTTCCAGTGAACCTTTTCAAGGGGCGCCCAACTGGGCGCTTGTAGCCCTTCTT 300

QY 301 GTCTTTGGGGGCTGCGCTGTGCTGAGAGTGAAGTCAAGAAATGAGGCTTTGGTGGGA 360
 DB 301 GTCTTTGGGGGCTGAGCTGTGTGAGTGAAGTCAAGAAAGATGGAACCACTGGTGGGA 360

QY 361 CAACTGACAGATTGGATGATGGCTTACCTGAGACACGCTGTGCTGATGATCACAAGC 420
 DB 361 CAACTGACAGAGTGGATGATGGCTTACCTGAGACGCGGCTGTGCTGATGATCACAAGC 420

QY 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGCGGAGCGGGCGCTTGGAGAGGCAAG 480
 DB 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGCGGAGCGGGCGCTTGGAGAGGCAAG 480

QY 481 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGCGGGGCGGTGGCACTG 540
 DB 481 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGCGGGGCGGTGGCACTG 540

QY 541 GGGGCGCTGATGATGATGAGGGGCTTTTGTCTAGCAAGTG 581
 DB 541 GGGGCGCTGATGATGATGAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 12
 ABR16642
 ID ABR16642 standard; DNA; 3542 BP.

AC ABR16642;
 DT 03-APR-2003 (first entry)
 DE Human bcl-2 gene SEQ ID No 4.
 KW Anti-tumour; DNzyme; bcl-2 gene; tumour; malignant; chemotherapy;
 KM radiation therapy; catalytic domain; enzyme; human; ds.
 OS Homo sapiens.
 PN WO200299090-A1.
 PD 12-DEC-2002.
 PF 07-JUN-2002; 2002MO-AU000739.
 PR 07-JUN-2001; 2001AU-00005527.
 (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 Sun L, Wang L, Turner RJ, Saravolac EG, Daes CR;
 WPI: 2003-140617/13.

XX Novel DNzyme useful for treating tumors, and for enhancing the
 PT sensitivity of malignant or virus infected cells to therapy, comprises a
 PT catalytic domain and binding domain contiguous to the catalytic domain.
 XX Disclosure: Page 44-45; 67P; English.

CC The invention relates to a DNzyme which specifically cleaves mRNA
 CC transcribed from a member of the bcl-2 gene family. The DNzymes comprise
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
 CC the catalytic domain, and therefore hybridise with, the two regions
 CC immediately flanking the purine residue of the cleavage site within the
 CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A
 CC pharmaceutical composition comprising a DNzyme of the invention is
 CC useful for treating tumors in a subject, and for enhancing the
 CC sensitivity of malignant or virus infected cells infected cells to
 CC therapy. The DNzymes are useful in diagnostics, therapeutics,
 CC prophylaxis, research agents and in kits. The DNzymes are also useful
 CC for increasing the susceptibility of tumour cells to anti-tumour
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide
 CC sequence represents a human bcl-2 gene of the invention

XX
 SQ Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 90.1%; Score 523.4; DB 7; Length 3542;
 Best Local Similarity 93.8%; Pred. No. 3.2e-130;
 Matches 545; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
 DB 177 ATGGCGACCCCGCTCAACCCAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 236

QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGCCCGCCGAC 120
 DB 237 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGCGCCAGCAGCTGAC 296

QY 121 CCGCTGACCAAGCATGCGGCTGCTGAGAGAGGTTTGAAGCCGTTTCCGCGCAC 180
 DB 297 CCGCTGACCAAGCATGCGGCTGAGAGATGATGTCGAGACCCGCTTCGCGCAC 356

QY 297 CCGCTGACCAAGCATGCGGCTGAGAGATGATGTCGAGACCCGCTTCGCGCAC 356
 DB 357 TTCTGTATCTGGGGCTCAGCTGATGTGACCCCAAGGCTCAGCAACGCTTCACC 416

QY 181 TTCTGTGACCTGGCGCTCAGCTACACGTGACCCCAAGGCTCAGCAACGCTTCACC 240
 DB 357 TTCTGTATCTGGGGCTCAGCTGATGTGACCCCAAGGCTCAGCAACGCTTCACC 416

QY 417 CAGGTTTCCAGCAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCAATTCTTT 300
 DB 301 GTCTTTGGGGGCTGCGCTGTGCTGAGAGTGTCAAAAGAAATGAGGCTTTGGTGGGA 360

QY 301 GTCTTTGGGGGCTGCGCTGTGCTGAGAGTGTCAAAAGAAATGAGGCTTTGGTGGGA 360
 DB 477 GTCTTTGGGGGCTGAGCTGTGTGAGAGTGTCAAAAGAGATGGAACCACTGGTGGGA 536

QY 477 GTCTTTGGGGGCTGAGCTGTGTGAGAGTGTCAAAAGAGATGGAACCACTGGTGGGA 536
 DB 361 CAACTGACAGATTGGATGATGGCTTACCTGAGACACGCTGTGCTGATGATCACAAGC 420

QY 537 CAACTGACAGAGTGGATGATGGCTTACCTGAGACGCGGCTGTGCTGATGATCACAAGC 596
 DB 537 CAACTGACAGAGTGGATGATGGCTTACCTGAGACGCGGCTGTGCTGATGATCACAAGC 596

QY 421 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGCGGAGCGGGGCGCTTGGAGAGGCAAG 480
 DB 597 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGCGGAGCGGGGCGCTTGGAGAGGCAAG 656

QY 597 AGTGGGGGCTGGGCGGAGTTCAACAGCTTATACGCGGAGCGGGGCGCTTGGAGAGGCAAG 656
 DB 481 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGAGGGGCGGTGGCACTG 540

QY 481 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGAGGGGCGGTGGCACTG 540
 DB 657 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGAGGGGCGGTGGCACTG 716

QY 657 CGTCTGCGGAGGAGGAGTGGGCAATCGGTGAGAGCAGTGTGAGAGGGGCGGTGGCACTG 716
 DB 541 GGGGCGCTGATGATGATGAGGGGCTTTTGTCTAGCAAGTG 581

QY 541 GGGGCGCTGATGATGATGAGGGGCTTTTGTCTAGCAAGTG 581
 DB 717 GGGGCGCTGATGATGATGAGGGGCTTTTGTCTAGCAAGTG 757

RESULT 13
 AAT96577
 ID AAT96577 standard; DNA; 583 BP.

```

AC AAT96577;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT 1..582
FT CDS /tag=a
FT /product="bcl-w"
XX
XX WO9735971-A1.
XX
XX 02-OCT-1997.
XX
XX 27-MAR-1997; 97WO-AU000199.
XX
XX 27-MAR-1996; 96AU-00008965.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Cory S, Adams JM, Gibson LM, Holmgren SP.
XX
XX WPI: 1997-489635/45.
XX
XX P-PSDB; AAW36047.
XX
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX inhibit cell survival, e.g. for treatment of cancer and degenerative
XX diseases.
XX
XX Claim 3; Page 48; 86pp; English.
XX
XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
XX family, extracted from an adult brain library. This gene promotes cell
XX survival, so its modulation is useful in treatment of cancer or auto-
XX immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
XX myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
XX immunodeficiency virus infection or in cell transplants. Up-regulation of
XX the gene can also be used to modify cell lines cultured in vivo, e.g. to
XX develop new lines, to facilitate isolation of hybridomas and to increase
XX survival of primary explants during genetic modification. It can be used
XX to produce recombinant Bcl-w for therapy, diagnosis, antibody production
XX or screening of potential modulators.
XX
XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 89.8%; Score 521.8; DB 2; Length 583;
XX Best Local Similarity 93.6%; Pred. No. 5e-130;
XX Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
XX
XX 1 ATGGCGACCCCGCCCTCAACCCAGACAGACGGGCTCTGAGCTTGTAGAGCTAT 60
XX 1 ATGGCGACCCCGCCCTCGGCCCCAGACAGACGGGCTCTGAGCTTGTAGAGCTAT 60
XX
XX 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGCTGAGCTGCGCCCTGGGAGAGCCAGCCGAGC 120
XX 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGCTGAGCTGCGCCCGGGAGAGGCCAGAGAGCTGAC 120
XX
XX 121 CCGCTGACCAACCAACCATGCGGGGCTGTGAGACGAGCTTTGAGACCCGTTCCGCGCACC 180
XX 121 CCGCTGACCAACCAACCATGCGGGGAGCTGAGATGAGTTCGAGACCCGCTTCGCGCACC 180
XX
XX 181 TTCTCTGAGCTGCGCCCTCAGCTACACGTGACCCCGAGGCTCCAGCAAGCGCTTCAAC 240
XX 181 TTCTCTGAGCTGCGCGGCTCAGCTGACGTGACCCCGAGGCTCAACGAGCAAGCGCTTCAAC 240
XX
XX 241 CAGGTTCCGACGACATTTTCCAAAGGGGCGCTTACCTGGGGCGGCTTGTGCAATCTTT 300
XX

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Db 241 CAGGTTCCGACGACATTTTCCAAAGGGGCCCCAATGCGGCCCGCTTGTAGCCTTCTT 300
QY 301 GTCCTTGGGGCTGCGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360
XX 301 CTTCTTTGGGGCTGCACTGTGTGTGAGTGTCAACAAGAGATGGAACCACTGTGGGA 360
Db 361 CAAGTGCAGAGTTGGATGTTGGCTTACCTGAGACACGCTCTGGCTACTGATCCACAGC 420
XX 361 CAAGTGCAGAGTGGATGTTGGCTTACCTGAGACACGCGGCTGTGATCCACAGC 420
Db 361 CAAGTGCAGAGTGGATGTTGGCTTACCTGAGACACGCGGCTGTGATCCACAGC 420
QY 421 AGTGGGGCTGCGGGGAGATTCAAGCTTATACGGGGAGCGGGGCCCTGGAGAGGCAAG 480
XX 421 AGTGGGGCTGCGGGGAGATTCAAGCTTATACGGGGAGCGGGGCCCTGGAGAGGCGGG 480
Db 481 CGTCTGCGGAGAGGGGAATCGGGCATCACTGTATACGGGGAGCGGGGCCCTGGAGAGG 540
XX 481 CGTCTGCGGAGAGGGGAATCGGGCATCACTGTATACGGGGAGCGGGGCCCTGGAGAG 540
QY 541 GGGGCCCTGTACTGTAGGGGCGCTTTTCTTGTAGCAAGTG 581
XX 541 GGGGCCCTGTACTGTAGGGGCGCTTTTCTTGTAGCAAGTG 581
Db
XX
XX RESULT 14
XX AAX25134
XX ID AAX25134 standard; DNA; 583 BP.
XX
XX AAX25134;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human bcl-w gene derivative.
XX
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
XX animal model; ss.
XX
XX Homo sapiens.
XX
XX WO9913710-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-AU000764.
XX
XX 16-SEP-1997; 97AU-00009228.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
XX WPI: 1999-243890/20.
XX
XX P-PSDB; AAY05532.
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX
XX Disclosure; Page 36; 52pp; English.
XX
XX The present sequence is described as a derivative of the human bcl-w gene
XX (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
XX member of the Bcl-2 family which is widely expressed and which is
XX essential for spermatogenesis. The invention relates generally to a
XX method of treatment and to an animal model for the identification of
XX molecules and genetic sequences useful for inducing or reducing fertility
XX of male animals. Methods are provided for the treatment of infertility,
XX or for reducing fertility, by modulating spermatogenesis. An animal model
XX carries a mutation in at least one allele of the human or murine bcl-w
XX gene or in a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no other
XX major abnormalities as determined by histological examination. They can
XX be used to screen for therapeutic molecules including genetic sequences
XX capable of inducing, enhancing or otherwise facilitating spermatogenesis
XX in animals, or which can induce infertility

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XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
 SQ
 Query Match 89.8%; Score 521.8; DB 2; Length 583;
 Best Local Similarity 93.6%; Pred. No. 5e-130;
 Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCTCAACCCAGACACACAGGGCTCTAGTGGTGAATTGTGGGCTAT 60
 DB 1 ATGGCGACCCAGCTCAACCCAGACACACAGGGCTCTAGTGGTGAATTGTGGGCTAT 60
 QY 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGAGCTGAGGAGAGGCGCCAGCCGAC 120
 DB 61 AAGCTGAGCAGAAAGGTTATGTCTGTGAGCTGAGCTGAGGAGAGGCGCCAGCCGAC 120
 QY 121 CCGCTGACCAAGCCTGAGCGGGCTGTGAGAGACAGATTGAGCCGTTTCCGCCGAC 180
 DB 121 CCGCTGACCAAGCCTGAGCGGGCTGTGAGAGACAGATTGAGCCGTTTCCGCCGAC 180
 QY 181 TTCTGTACCTGGCGCTGAGCTACAGTGAACCCAGGCTGAGCCAGCAAGCTTCAAC 240
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RESULT 15
 AAV28334
 ID AAV28334 standard; cDNA; 579 BP.
 AC AAV28334;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Human bcl-y gene.
 XX
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..579
 FT /tag= a
 FT /product= "bcl-y"
 FT /note= "No stop codon given"
 XX
 PN US5789201-A.
 XX
 PD 04-AUG-1998.
 XX
 PF 11-FEB-1997; 97US-00798897.

XX
 PR 23-FEB-1996; 96US-0012201P.
 XX
 PA (COCE-) COCENSYS INC.
 XX
 PI Guastella J;
 XX
 DR WPI: 1998-446079/38.
 DR P-PSDB; AAM61392.
 XX
 PT Nucleic acid encoding B-cell lymphoma-Y protein - useful for producing
 PT recombinant protein for use in treating uncontrolled cell growth e.g.
 PT cancers.
 PS Claim 3; Column 15/16; 27pp; English.
 CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
 CC family, components in the cell death pathway. The bcl-2 family have both
 CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
 CC the apoptosis activity category. The recombinant protein may be used to
 CC prevent uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired
 CC
 XX
 SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;
 Query Match 89.2%; Score 518.2; DB 2; Length 579;
 Best Local Similarity 93.4%; Pred. No. 4.6e-129;
 Matches 541; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Thu Mar 4 08:13:37 2004

us-09-508-745-3.rng

Page 12

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 200000000

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Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	561.4	96.6	579	2	US-08-978-523-1
3	518.2	89.2	579	1	US-08-798-897-2
4	518.2	89.2	579	2	US-08-978-523-2
5	376	64.7	1098	4	US-09-010-147B-23
6	375.6	64.6	1864	4	US-09-149-476-130
7	133	22.9	926	1	US-08-081-448-5
8	133	22.9	926	2	US-08-470-670A-6
9	133	22.9	926	3	US-08-481-739-1
10	133	22.9	926	3	US-09-167-921-1
11	133	22.9	926	3	US-09-277-020-39
12	133	22.9	926	3	US-09-323-743-1
13	133	22.9	926	4	US-08-461-511A-6
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ALIGNMENTS

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RESULT 1
US-08-798-897-1
Sequence 1, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-1
Query Match 96.6%; Score 561.4; DB 1; Length 579;
Best Local Similarity 98.1%; Pred. No. 5,1e-145;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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US-08-978-523-1
Sequence 1, Application US/0878523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmund, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-1
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Query Match 96.6%; Score 561.4; DB 2; Length 579;
Best Local Similarity 98.1%; Pred. No. 5.1e-145;
Matches 568; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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RESULT 3
US-08-798-897-2
Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-2

Query Match 89.2%; Score 518.2; DB 1; Length 579;
Best Local Similarity 93.4%; Pred. No. 3.8e-133;
Matches 541; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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RESULT 4
US-08-978-523-2
Sequence 2, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-2

Query Match 89.2%; Score 518.2; DB 2; Length 579;
Best Local Similarity 93.4%; Pred. No. 3.8e-133;
Matches 541; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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RESULT 5

US-09-010-147B-23
; Sequence 23, Application US/09010147B
; Patent No. 6653445

GENERAL INFORMATION:

APPLICANT: Nt et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-NO. 6653445-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997

APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF353

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

Query Match 64.7%; Score 376; DB 4; Length 1098;
Best Local Similarity 91.9%; Pred. No. 5,5e-94;
Matches 397; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCCAAGCTCAACCCAGACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120
DB 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGAGCTGGCCGCGGGAAGGCCAGAGCTGAC 120
QY 121 CCGCTGCACCAAGCCATGGGGCTGTGAGAGAGAGTTGAGAACCCGTTTCCGCGGCACC 180

DB 121 CCGCTGCACCAAGCCATGGGGCTGTGAGAGAGAGTTGAGAACCCGTTTCCGCGGCACC 180
QY 181 TTCTGTACCTGGGCGGCTCAGCTACAGTGAACCCAGGCTCAGCCACAAAGCTTAC 240
DB 181 TTCTGTACCTGGGCGGCTCAGCTACAGTGAACCCAGGCTCAGCCACAAAGCTTAC 240
QY 241 CAGGTTTCCGACGAATTTCCTTCCAGAGGGGCGCTTACTGAGGCGCTTGTGACATTCCTT 300
DB 241 CAGGTTTCCGACGAATTTCCTTCCAGAGGGGCGCTTACTGAGGCGCTTGTGACATTCCTT 300
QY 301 GTCTTTGGGCGCTCCCTGTGTGCTGAGAGTGTCAAAGAAATGAGACCTTTGGTGGGA 360
DB 301 GTCTTTGGGCGCTCCCTGTGTGCTGAGAGTGTCAAAGAAATGAGACCTTTGGTGGGA 360
QY 361 CAAGTCAGAGAGTGGATGTGGTGGCCCACTGGAGACAGCTGGGCTGACTGATCCAGAC 420
DB 361 CAAGTCAGAGAGTGGATGTGGTGGCCCACTGGAGAGAGCTGGGCTGACTGATCCAGAC 420
QY 421 AGTGGGGGCTGG 432
DB 421 AGTGGGGGCTGG 432

RESULT 6

US-09-149-476-130
; Sequence 130, Application US/09149476
; Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584

[illegible]

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 64.6%; Score 375.6; DB 4; Length 1864;
Best Local Similarity 91.7%; Pred. No. 8,5e-94;
Matches 396; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCTCAACCCAGACACACGCGCTCTAGTGGCTGATCTTTAGGCTAT 60
DB 11 ATGGGACCCCGAGCTCAACCCAGACACACGCGCTCTAGTGGCTGATCTTTAGGCTAT 70
QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGCGCTTGGGGAAGGCCAGCCGAC 120
DB 71 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGCGCTTGGGGAAGGCCAGCCAGCTGAC 130
QY 121 CCGCTGACACAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGGAC 180
DB 131 CCGCTGACACAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGGAC 190
QY 181 TTCTCTGACCTGCGCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAACGCTTCA 240
DB 191 TTCTCTGATCTGCGCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAACGCTTCA 250
QY 241 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAACCTGGGGCCGTTCTGTGCAATCTTT 300
DB 251 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAACCTGGGGCCGCTTGTACCTTTCTT 310
QY 301 GCTTTGGGGGCTCCCTGTGTCTGAGATGTCAACAAAGAAATGAGCTTTGGTGGGA 360
DB 311 GCTTTGGGGGCTCCCTGTGTCTGAGATGTCAACAAAGAAATGAGCTTTGGTGGGA 370
QY 361 CAGGTCAGAGATGATGATGATGCTTACCTGAGAGACAGCTGCTGATGATCCAGAC 420
DB 371 CAGGTCAGAGATGATGATGATGCTTACCTGAGAGACAGCTGCTGATGATCCAGAC 430
QY 421 AGTGGGGGCTGG 432
DB 431 AGTGGGGGCTGG 442

RESULT 7
US-08-081-448-5
Sequence 5, Application US/08081448
Patent No. 5646008

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago

STATE: IL
COUNTRY: USA
ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448

FILING DATE: 19930622
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.

REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 135..836

US-08-081-448-5

Query Match 22.9%; Score 133; DB 1; Length 926;
Best Local Similarity 58.0%; Pred. No. 2.9e-27;
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGCTCTGTGAGACGAGTTTGAACCCGTTTCCGCGGACCTTCTG 187
DB 394 AGCAAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
QY 188 ACCTGCGGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTCAACCCAGGTTT 247
DB 454 ACTTGACATCTCCAGCTCAGCTACATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
QY 248 CCGAGCACTTTTCCAGAGGGGGCCCTTAACCTGGGGCCGTTCTGTGCAATCTTTGCTTTG 307
DB 514 TGAATGAATCTTCCGAGGAGTGGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 573
QY 308 GGGCTGCTGTGTCTGAGAGTGTCAACAAAGAAATGAGCTTTGGTGGGACAGTGC 367
DB 574 GCGGGGCACTGTGCTGAGAAAGCGTGAACAGAGAGTACAGTATGATGAGTGGATG 633
QY 368 AGGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 427
DB 634 CAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
QY 428 GCTGGCGGAGTTCAACAGCTCTATACGGGAGCGGGGCCCTTGAAGAGGAGGAGGAGGAG 487
DB 694 GCTGGGATATCTTTGTGATCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 753
QY 488 GGGAGGGAAGTGGGATCAGTGAAGAGAGATGCTGACCGGGGGCCG 532
DB 754 AGGAAGCTTCAACCGCTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 798

RESULT 8
US-08-470-670A-6
Sequence 6, Application US/08470670A
Patent No. 5834309

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: Texas
COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ACD:090--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-470-670A-6

Query Match      22.9%; Score 133; DB 2; Length 926;
Best Local Similarity 58.0%; Pred. No. 2.9e-27;
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGAGAGAGATTGAGACCCGTTCCGCCGACCTTCTCTG 187
    |||||
DB 394 AGCAAGCGCTGAGGAGAGAGAGAGAGAGATTGAGACCGGTTGACCGGCGGACCTTCACTG 453
QY 188 ACTGCGCGCTGACGTACAGGTGACCCGAGCTGACCCGACCAAGCTTCAACGAGTTT 247
    |||||
DB 454 ACTGACATCCACGCTCCACATCACCCGAGGACAGCATATCAGAGCTTTGAAACAGGTAG 513
QY 248 CCGACGAACCTTTTCAAGGGGGCCCTTAAGCTGGGGCCGCTTGTGGCATTTCTTGTCTT 307
    |||||
DB 514 TGAATGAACCTTCCGGGATGGGGTAAACCTGGGGTCCGATTGTGGCCCTTTTCTCTTCG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGGTGCAACAAGAAATGAGACCTTTGGTGGGACAAAGTC 367
    |||||
DB 574 GCGGGGCACTGTGTGAGAAAGCGTAGACAGAGAGATGAGATGTTGGTGTGATGCG 633
QY 368 AGAATTGATGTGCGCTTACCTTGAGACACGTCTGCTGATGATCCACAGCAGTGGGG 427
    |||||
DB 634 CAGCTTGATGGCAGCACTTACCTGAATGACACCTTAGAGCCTTGGATCCAGAGAAAGCGCG 693
QY 428 GCTGGGCGGAGTTCAAGCTTATACGGGGACGGGGCCCTTGAAGAGGACAGCGCTCTGC 487
    |||||
DB 694 GCTGGGATACCTTTTGTGAACTCTATGTGGAACAATGCGACGCCGAGAGCCGAAAGGCGC 753
QY 488 GGGAGGGGAACCTGGGCATCAGTGAGACAGTGTCTGACGGGGGCGG 532
    |||||
DB 754 AGGAACGCTTCAACCGCTGTTCTTGACGGGACATGATGTGGCGG 798

RESULT 9
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
```

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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-4214
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

Query Match      22.9%; Score 133; DB 3; Length 926;
Best Local Similarity 58.0%; Pred. No. 2.9e-27;
Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGAGAGAGATTGAGACCCGTTCCGCCGACCTTCTCTG 187
    |||||
DB 394 AGCAAGCGCTGAGGAGAGAGAGAGAGAGATTGAGACCGGTTGACCGGCGGACCTTCACTG 453
QY 188 ACTGCGCGCTGACGTACAGGTGACCCGAGCTGACCCGACCAAGCTTCAACGAGTTT 247
    |||||
DB 454 ACTGACATCCACGCTCCACATCACCCGAGGACAGCATATCAGAGCTTTGAAACAGGTAG 513
QY 248 CCGACGAACCTTTTCAAGGGGGCCCTTAAGCTGGGGCCGCTTGTGGCATTTCTTGTCTT 307
    |||||
DB 514 TGAATGAACCTTCCGGGATGGGGTAAACCTGGGGTCCGATTGTGGCCCTTTTCTCTTCG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGGTGCAACAAGAAATGAGACCTTTGGTGGGACAAAGTC 367
    |||||
DB 574 GCGGGGCACTGTGTGAGAAAGCGTAGACAGAGAGATGAGATGTTGGTGTGATGCG 633
QY 368 AGAATTGATGTGCGCTTACCTTGAGACACGTCTGCTGATGATCCACAGCAGTGGGG 427
    |||||
DB 634 CAGCTTGATGGCAGCACTTACCTGAATGACACCTTAGAGCCTTGGATCCAGAGAAAGCGCG 693
QY 428 GCTGGGCGGAGTTCAAGCTTATACGGGGACGGGGCCCTTGAAGAGGACAGCGCTCTGC 487
    |||||
DB 694 GCTGGGATACCTTTTGTGAACTCTATGTGGAACAATGCGACGCCGAGAGCCGAAAGGCGC 753
QY 488 GGGAGGGGAACCTGGGCATCAGTGAGACAGTGTCTGACGGGGGCGG 532
    |||||
DB 754 AGGAACGCTTCAACCGCTGTTCTTGACGGGACATGATGTGGCGG 798

RESULT 10
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
```

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1  APPLICANT: Zhang, Qinqiong
2  TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
3  FILE REFERENCE: ISPh-0324
4  CURRENT APPLICATION NUMBER: US/09/167,921A
5  CURRENT FILING DATE: 1998-10-07
6  NUMBER OF SEQ ID NOS: 50
7  SOFTWARE: PatentIn Ver. 2.0
8  SEQ ID NO 1
9  LENGTH: 926
10 TYPE: DNA
11 ORGANISM: Homo sapiens
12 FEATURE:
13 NAME/KEY: CDS
14 LOCATION: (135)..(836)
15 PUBLICATION INFORMATION:
16 DATABASE ACCESSION NUMBER: L20121 Genbank
17 DATABASE ENTRY DATE: 1994-07-26
18 US-09-167-921-1

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Query Match	22.9%;	Score 133;	DB 3;	Length 926;
Best Local Similarity	58.0%;	Pred. No. 2.9e-27;		
Matches 235; Conservative	0;	Mismatches 170;	Indels 0;	Gaps 0

QY	128	ACCAAGCATGCGGGGCTGCTGGAGAGAGACTTTGAAACCGTTTCGCGCGCACCTTCTCTG	1.87
Db	394	AGCAAGCGCTGAGGGAGGACGAGCGACGAGTTTGAATCTGGTACCGCGGGCATTTCAAGTG	4.53
QY	188	ACCTGGCCGCTCAGTCAACGTGACCCCGAGTCCAGCCAGCAACGTTCAACCCAGGTTT	2.47
Db	454	ACCTGACATCCGAGCTTCCATCACCCCGGACGACATTCAGAGCTTTGAAACAGGTAG	51.31
QY	248	CCGACGAACTTTTCCAAAGGGGGCCCTAATGGGGCCGCTTGTGGCAATCTTTGTCTTTG	3.07
Db	514	TGATGAACCTTTCGCGGATGGGGGTAACTGGGGGTGCAATGTGTGCGCTTTTTCCTTTCG	5.73
QY	308	GGGCGTCCCTGTTGTGTGAGGTGCAACAAAGAAATGAGGCTTTGGTGGGACAAATGC	3.67
Db	574	GCGGGGCACTGTCCGTGGAAAGGTGTGACAAAGAAATGAGATTTGGTGTGATCG	63.33
QY	368	AGGATTTGATGTGTGGCTTACCTGGAGACACGTCTGGCTGACTGTGATCCACAGCAGTGGGG	4.27
Db	634	CAGCTTGGATGGGCCACTTACCTGAAATGACACCACTTGAGCCTTGGATTCGAGGAAACGGCG	6.93
QY	428	GCTGGGCGAGTTCACAGCTCTAATACGGGGACGGGACCCTGGAGGAGCAAGCGCTTGC	4.87
Db	694	GCTGGGATTACTTTTGTGGAACCTTAATGGGAAACAATGACAGACGACGAGCGGAAAGGGCC	75.31
QY	488	GGGAGGGGAACTGGGATCATGTAGGAGACAGTCTGACGGGGCCG	5.32
Db	754	AGGAACGCTTCAACCGCTGGTCTTCAGCGGGCANTAACTGTGGCCG	7.98

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RESULT 11
US-09-277-020-39
: Sequence 39, Application US/09277020
: Patent No. 6210892
:
: GENERAL INFORMATION:
: APPLICANT: Bennett, C. Frank
: TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
: FILE REFERENCE: ISPN-0339
: CURRENT APPLICATION NUMBER: US/09/277,020
: CURRENT FILING DATE: 1999-03-26
: EARLIER APPLICATION NUMBER: 09/167,921
: EARLIER FILING DATE: 1998-10-07
: NUMBER OF SEQ. ID NOS.: 65
: SOFTWARE: patentIn Ver. 2.0
: SEQ. ID NO. 39
: LENGTH: 926
:
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-277-020-39

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Query Match	22.9%;	Score 133;	DB 3;	Length 926;
Best Local Similarity	58.0%;	Pred. NO. 2.9e-27;		
Matches 235; Conservative	0;	Mismatches 170;	Indels 0;	Gaps 0;

Qy	120	ACCAACAGCAGGGGGGTGTGTGGAGACAGATTGGAGACCGGTTTCCGGCCGACCTTCTGTG	187
Ds	394	AGCAACGGCTGAGGAGGAGCAGCGACGAGTTTGAACACGCGTACCGGCGGGCATTCAGTG	453
Qy	188	ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCAGCAACGCTTGACCCAGGTTT	247
Ds	454	ACCTGACATCCAGCTCCACATCACCCAGGAGACGATATCAGAGCTTTGAACAGGTAG	513
Qy	248	CCGACGAACCTTTTCCAAAGGGGCGCTTAACCTGGGGCCGTCCTTGTGGCAATCTTTGTCTTTG	307
Ds	514	TGAATGAACCTCCGGGGATGGGGTAACTGGGGGTGCAATTGTGGCTTTTCTTCCTCG	573
Qy	308	GGGCTCCCGTGTGTGTGTGAGTGTCAACAAAGAAATGGAGCCTTTGCTGGGACAAAGTGC	367
Ds	574	GCGGGGCACCTGTGCCTGGGAAACCGTAGACAAAGAGATGCAGATTTGTGTGCGATCG	633
Qy	368	AGGATTGATGTGTGTGCTTACTGTGAGACACGCTCTGTGCTGATCGATCCAGACGATGGGG	427
Ds	634	CAGCTTGGATGGCCACTTACCTGGAATGACACACTAGAGCCTTGGATTCAGAGAAAGCGCG	693
Qy	428	GCTGGGCGGAGTTCACAGCTTAAACGCGGAGCGGGGCCCTGGAGAGAGGCAACGGCTTCG	487
Ds	694	GCTGGGATCTTTTGTGGAACTCTATGGGAAACAATGTGACGACGCGAGACGCCGAAAGGCC	753
Qy	488	GGGAGGGGAACCTGGGCATCAGTAGAGACAGTGTGACGGGGCGCG	532
Ds	754	AGGAACGCTTACACCGCTGGTTCCTGACGGGCATGACCTGTGGCGG	798

RESULT 12 743-743-1
US-09-323-743-1
Sequence 1, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nicholoff, Brian J.
APPLICANT: Zhang, Qingqing
TITLE OF INVENTION: Antisense Modulation of
FILE REFERENCE: 15PH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATE: 1994-07-26
US-09-323-743-1

Query	March 22.9%	Score 133	DB 3;	Length 926;
Best Local Similarity	58.0%	Pred. No. 2.9e-27;		
Matches 235; Conservative	0;	Mismatches 170;	Indels 0;	Gaps 0
OY	128	ACCAAGCCATCGGCGCTCTGTGAGACGACGTTTGAGACCCGTTTCGCGCGCACCTTCCTCG	187	
Db	394	AGCAAGCCCTAGGAGGACGACGACGCGAGTTTGAACTCGGATCCGCGCGGCGCATTCAGTG	453	

DB 634 CAGCTTGATGGCCACTTACCTGATGACCACTAGAGCTTGATCCAGAGAACGGCG 693
QY 428 GCTGGCGGAGCTTCACAGCTCTATACGGGAGCGGGCCCTGAGAGAGCAGCGCTTGC 487
DB 694 GCTGGGATACCTTTGTGTGAACCTCTATGGACATGACAGCAGCCGAAAGGCGC 753
QY 488 GGGAGGGGAACCTGGGATCATGAGAGACAGTGTGACGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGATATCTGTGCGG 798

RESULT 15

US-09-023-655-1430
; Sequence 1430, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: word Perfect 6.1 for windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1430:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9510900
; US-09-023-655-1430

Query Match 22.9%; Score 133; DB 4; Length 926;

Best Local Similarity 58.0%; Pred. No. 2.9e-27;

Matches 235; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGCTGAGAGCACTTTGAGACCCGTTTCGCGCACCTTCTTG 187
DB 394 ACCAAGCCGCTGAGGAGGAGCGAGGAGTTGAACTGCGGTACCGCGGCGATTCAGTG 453
QY 188 ACTTGCGCGCTCAGCTACGCTGACCGCCAGGCTCAGCCGACGAGGTTT 247
DB 454 ACTGACATCCAGCTCCACATCACCCGAGGACAGCATATCAGAGCTTTGAACAGGTAG 513

QY 248 CCGACGAATTTTCCAAAGGGGCCCCCTTAACGTGGGCGCTTGTGCAATTTTGTCTTTG 307
DB 514 TGAATGAACCTTCCGGGATGGGGTAACTGGGGTGCATTTGTTCCTTTCG 573
QY 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGACAAGTGC 367
DB 574 GCGGGGCACTGTGTGCTGAAAGCGTAAACAAGAGATGCAAGTATTTGTGAGTCGATCG 633
QY 368 AGGATTGATGATGGCCCTACCTGGAGACACGCTGTGCTGATCCACAGACAGTGGGG 427
DB 634 CAGCTTGATGCGCCACTTAACCTGAATGACACCTAGAGCCTTGATCCAGAGAAAGCGCG 693
QY 428 GCTGGCGGAGTTCAACGCTTATACGGGAGCGGGCCCTGAGAGGACAGCGCTTGC 487
DB 694 GCTGGGATACCTTTGTGTGAACCTCTATGGGAACTAATGACAGCCGAGCGAAAGGCGC 753
QY 488 GGGAGGGGAACCTGGGATCATGAGAGAGATGCTGACGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGATATCTGTGCGG 798

Search completed: March 3, 2004, 18:38:47
Job time : 87 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2004, 16:13:49 ; Search time 3188 seconds
(without alignments)
5442.261 Million cell updates/sec

Title: US-09-508-745-3

Perfect score: 581
Sequence: 1 atggcgagccagcagctcaac.....gccttttctgctagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_est1:*
10: gb_est2:*
11: gb_hci:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_rhg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	582	29	AY421022 Mus muscu
2	581	100.0	1949	11	AK015644 Mus muscu
3	581	100.0	3487	11	AK004680 Mus muscu
4	579.4	99.7	969	13	BY715200 BY715200

5	524.4	90.3	967	13	BU503850
6	521.8	89.8	582	29	AY421020
7	498.4	85.8	804	9	AL157542
8	497.8	85.7	1030	10	BE793530
9	448.2	77.1	815	10	BF785386
10	433.8	74.7	697	12	B1770566
11	433	74.5	854	11	AK013244
12	420.2	72.3	792	12	BG298789
13	418.6	72.0	623	14	CB578463
14	414.8	71.4	540	10	AM258810
15	395	68.0	626	14	CA391923
16	370	63.7	643	12	B1910270
17	360	62.0	440	14	CB749817
18	354.8	61.1	559	13	BY704881
19	351.8	60.6	437	14	CB790932
20	342	58.9	548	14	CF533813
21	336.2	57.9	869	13	BU557268
22	336.2	57.9	872	13	BU557410
23	331.8	57.1	548	14	CA407899
24	330.2	56.8	645	13	BY740551
25	327	56.3	362	9	AA596919
26	314.8	54.2	410	14	CB804140
27	309.6	53.3	460	13	BY285647
28	304.4	52.4	449	13	BY253191
29	295.8	50.9	327	29	AY421021
30	295	50.8	1053	13	BU931540
31	288.4	49.6	758	12	B1764428
32	279	48.0	457	10	BB856021
33	275	47.3	430	14	CB760687
34	271.6	46.7	425	13	BY251598
35	268.6	46.2	467	13	BY253189
36	265.4	45.9	302	13	BY356166
37	263.8	45.4	305	13	BY356183
38	255.8	44.0	749	12	BG677345
39	254	43.7	353	13	BY312773
40	250	43.0	601	10	BF204905
41	248	42.7	375	13	BY302913
42	247.4	42.6	1064	13	BQ646339
43	246	42.3	372	13	BY133304
44	245.2	42.2	452	14	CB786193
45	244.8	42.1	314	13	BY356000

ALIGNMENTS

RESULT 1
LOCUS AY421022
DEFINITION Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY421022
VERSION AY421022.1 GI:39776979
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission

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Location/Qualifiers
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/clone="4930488D08"
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ORIGIN

Query Match 100.0%; Score 581; DB 11; Length 1949;
Best Local Similarity 100.0%; Pred. No. 2,4e-135;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 132 ATGGCGACCCCAAGCTTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 191
QY 61 AAGCTGAGGAGGAGGGTATATGTCGTGAGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120
Db 192 AAGCTGAGGAGGAGGGTATATGTCGTGAGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 251
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTTCCGCGCAC 180
Db 252 CCGCTGACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAAGACCCGTTTCCGCGCAC 311
QY 181 TTCTCTGACCTGGCCGCTCACTACAGTGAACCCAGGCTCAAGCCAGAACGCTTAC 240
Db 312 TTCTCTGACCTGGCCGCTCACTACAGTGAACCCAGGCTCAAGCCAGAACGCTTAC 371
QY 241 CAGGTTTCCGACGAAGTTTCCAGAGGGGGCCCTAAGTGGGGCGTCTGTGGCAATTC 300
Db 372 CAGGTTTCCGACGAAGTTTCCAGAGGGGGCCCTAAGTGGGGCGTCTGTGGCAATTC 431
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QY 361 CAAGTGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGGCTGACTGATTCACAGC 420
Db 492 CAAGTGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGGCTGACTGATTCACAGC 551
QY 421 AGTGGGGGGCTGGGGGAGATTACAGCTCTATACGGGGAGCGGGGCGCTGGAGAGAGCAG 480
Db 552 AGTGGGGGGCTGGGGGAGATTACAGCTCTATACGGGGAGCGGGGCGCTGGAGAGAGCAG 611
QY 481 CGTCTGGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGGCGTGGCACTG 540
Db 612 CGTCTGGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGGCGTGGCACTG 671
QY 541 GGGGCGCTGTGTAAGTGAAGGCGCTTTTCTTCTAGCAAGTG 581
Db 672 GGGGCGCTGTGTAAGTGAAGGCGCTTTTCTTCTAGCAAGTG 712

RESULT 3

AK004680
LOCUS 3487 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched
library, clone:1200009124 product:Bcl2-1like 2, full insert
sequence.
ACCESSION AK004680
VERSION AK004680.1 GI:12836027
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaibiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Matshiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 11076861
REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Yamamatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.c.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.

DB 190 AAGTGAAGGCAAGAGGTTATGTCTGTGAGCTGGCCCTCGGGAGAGCCCAAGCCCGAC 249
QY 121 CCGCTGACCAAGCCATGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 180
DB 250 CCGCTGACCAAGCCATGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 309
QY 181 TTCTGACCTGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 240
DB 310 TTCTGACCTGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 369
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DB 370 CAGTTTCCGAGCAATTTTCCAGGGGCGCTTAACTGGGCGCTTGTGCAATTTCTT 429
QY 301 GTCTTTGGGCGCTGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 360
DB 430 GTCTTTGGGCGCTGCGGCTCTGTGAGACAGATTGAGACCCCTTTCCGCGAC 489
QY 361 CAAGTGAAGGATTGATGATGAGCTGA-CCTGAGACACAGTGTGCTGATGATGATG 419
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QY 478 CCGCTGCGGCGCTGCGGCGCTTAACTGGGCGCTTGTGCAATTTCTT 536
DB 610 CCGCTGCGGCGCTGCGGCGCTTAACTGGGCGCTTGTGCAATTTCTT 669
QY 537 ACTGGGGCGCTGCTGATGATGATGAGCTGA-CCTGAGACACAGTGTGCTGATGATG 581
DB 670 ACTGGGGCGCTGCTGATGATGATGAGCTGA-CCTGAGACACAGTGTGCTGATGATG 715

RESULT 6
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LOCUS Homo sapiens BCL2L2 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.U.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.

FEATURES
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ORIGIN
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Query Match 89.8%; Score 521.8; DB 29; Length 582;
Best Local Similarity 93.6%; Pred.No. 1.1e-120;
Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCTCAACCCAGACACAGGCGCTAGTGGCTAGTCTTTAGAGCTAT 60
DB 1 ATGGGACCCCGAGCTCAACCCAGACACAGGCGCTAGTGGCTAGTCTTTAGAGCTAT 60
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DB 61 AAGCTGAGCAGAAAGGTTATGTCGTGAGCTGAGCTGCGGAGGAGGAGCCAGCTTAC 120
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DB 121 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGATTGAGACCCCTTTCCGCGAC 180
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DB 541 GGGGCGCTGCTGATGATGATGAGCTGA-CCTGAGACACAGTGTGCTGATGATG 581

RESULT 7
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LOCUS DKFZP610D0816.r1.761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKFZP610D0816.5, mRNA sequence.
ACCESSION AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 804)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrate; Euteleostomi;
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.U.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.

MIPS
Institute Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL European Molecular Biology Laboratories,
Heidelberg/Germany within the cDNA sequencing consortium of the

German Genome Project.
No sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES
source

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/clone="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"
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ORIGIN

Query Match 85.8%; Score 498.4; DB 9; Length 804;
Best Local Similarity 93.3%; Pred. No. 1e-114;
Matches 542; Conservative 0; Mismatches 37; Indels 2; Gaps 2;

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QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 60
DB 134 ATGGCGACCCAGCCTCGGCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 193
QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120
DB 194 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTAC 253
QY 121 CCGCTGACCAAGGCATCGGGCTGCTGAGACGAGTTTGAAGACCGCTTCCGCGCACC 180
DB 254 CCGCTGACCAAGGCATCGGGCTGCTGAGACGAGTTTGAAGACCGCTTCCGCGCACC 313
QY 181 TTCTCTGACTGCGCGCTCAGCTACACGCTGACCCAGGCTCAGCCAGCAACGCTTACC 240
DB 314 TTCTCTGACTGCGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTACC 373
QY 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
DB 374 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 433
QY 301 GTCTTTGGGGCTGCGCGCTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
DB 434 GTCTTTGGGGCTGCACTGTGTGACGAGAGTGTCAACAAGAGATGAACTAGTGGGA 493
QY 361 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 494 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
QY 421 AGTGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGGACGGGGCGCTGAGAGGACGCG 480
DB 554 AGTGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGGACGGGGCGCTGAGAGGACGCG 612
QY 481 CGTCTGCGGAGGGGGAATGCGGCATCAGTGAAGGACAGTGTGACGCGGGCGCTGCACTG 540
DB 613 CGTCTGCGGAGGGGGAATGCGGCATCAGTGAAGGACAGTGTGACGCGGGCGCTGCACT- 671
QY 541 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
DB 672 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 712
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RESULT 8
BE793530
LOCUS 601590016r1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
DEFINITION mRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1030)
NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM800 row: P column: 04
High quality sequence start: 5
High quality sequence stop: 709.

FEATURES
source

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1..1030
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="MDH10B (phage-resistant)"
/clone.lib="NIH_MGC_7"
/clone="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 85.7%; Score 497.8; DB 10; Length 1030;
Best Local Similarity 91.0%; Pred. No. 1.7e-114;
Matches 529; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 60
DB 144 ATGGCGACCCAGCCTCGGCCAGACACACGGGCTTAGTGCTGACTTTGTAGGCTAT 203
QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120
DB 204 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 263
QY 121 CCGCTGACCAAGGCATCGGGCTGCTGAGACAGAGTTTGAAGACCGCTTCCGCGCACC 180
DB 264 CCGCTGACCAAGGCATCGGGCTGCTGAGACAGAGTTTGAAGACCGCTTCCGCGCACC 323
QY 181 TTCTCTGACTGCGCGCTCAGCTACACGCTGACCCAGGCTCAGCCAGCAACGCTTACC 240
DB 324 TTCTCTGACTGCGCGCTCAGCTGATGTATACCCAGGCTCAGCCAGCAACGCTTACC 383
QY 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
DB 384 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 443
QY 301 GTCTTTGGGGCTGCGCGCTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
DB 444 GTCTTTGGGGCTGCACTGTGTGACGAGTGTCAACAAGAGATGAACTAGTGGGA 503
QY 361 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 504 CAAGTGCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 563
QY 421 AGTGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGACGGGGCGCTTGGAGAGGACGCG 480
DB 564 AGTGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGACGGGGCGCTTGGAGAGGACGCG 623
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QY	Db	QY	Db	RESULT 9	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
481	624	541	684	BF785386	BF785386	602111728p1	BF785386	BF785386	EST.	Mus musculus	Mus musculus	Enkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	NIH-MGC	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.
CGCTGTCGGAGAGGGGAATCTGGGCATCACTGAGAGCAGTGTACCGGGGGCCTGGCACTG	CGTCTCGCGGAGAGGGGACTGTGGGCATCACTGAGAGCAGTGTCTGTACCGGGGGCCTGGCACTG	GGGGCCCTGTGTAACCTGTAGGGGCGCTTTTGTCTAGCAAGTG	GGGGGCGCTGGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG	815 bp	mRNA	linear	EST 12-JAN-2001	GI:12090422								

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
 Plate: L14M853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.
 Location/Qualifiers
 1..815

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4239798"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NCI_CGAP_Kid44"
/notes="Organ Kidney; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dI Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

```

Query Match	77.1%;	Score 448.2;	DB 10;	Length 815;
Best Local Similarity	96.9%;	Pred. NO. 4.8e-102;		
Matches 532; Conservative	0;	Mismatches 8;	Indels 9;	Gaps 7

[illegible]

Db	240	CCAAAGGGGGCCCTAACTGGGGCCGCTTGTGGCATTC	---	TGTC	TGGGGCGTGCCTGTG	296
Qy	321	TGCTGAGGTGTCAACAAAGAAATG	BACACTT	TGGTGGAACA	GTGCAGATTTG	380
Db	297	TGCTGAGGTGTCAACAAAGAAATG	BACCC	-TTG	ATGGGACAATGCAGGATTTG	355
Qy	381	GGCCTACCTGGAGACACGCTTG	GGCTGATCTG	GCATCACACAGCA	GTGGGGGCTGGGCGGAGTT	440
Db	356	GGCCTACCTGGAGACACGCTTG	GGCTGATCTG	GCATCACACAGCA	GTGGGGGCGTGGGCGGAGTT	415
Qy	441	CACAGCTCTATACGGGGACGGGG	CCCTTG	AGAGGACCGG	CGCTCTTGCGGGAGGGGAC	500
Db	416	CACAGCTCTATACGGGGGACGGGG	CCCTTG	AGAGGACCGG	-GCTTGCGGGAGGGGAAAC	473
Qy	501	GGCATCAATGAGACAGTGTCTGA	CCGGGGCGGTGG	CAC	TGGGGGGCGCTGGTAAC	560
Db	474	GGCATCAATGAGGACAGTGTCTGA	CCGGGGCGCGTGG	CACT	-GGGGCGCTGGTAAC	532
Qy	561	GGCCTTTT	569			
Db	533	GGCCTTTT	541			

RESULT	10
LOCUS	B1770566
DEFINITION	B1770566 697 bp mRNA linear EST-25-SEP-2001 60306036221 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5' , mRNA sequence.
ACCESSION	B1770566
VERSION	B1770566
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 697)	NIH-MGC	http://mgc.nci.nih.gov/	
		National Institutes of Health,	Mammalian Gene Collection (MGC)	
		Unpublished. (1999)		
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapds-1@mail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: L14M1526	row: k	column: 15	
	High quality sequence start: 21			
	High quality sequence stop: 695.			

FEATURES

source

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ORIGIN
Query Match
74.7%, Score 433.8; DB 12; Length 697;

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5209863"
/lab_host="MDH10B"
/clone_1lb="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: PCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lungs; 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

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(MGDI:108052)
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 /db_xref="GI:12850488"
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 GAALCAESVINKEMEPVGVDDMMVAAYLETFLADWIHSSGGVNRSSQLLSASLYKVG
 LHGKTGPLMGCMGACNRG"

ORIGIN

Query Match 74.5%; Score 433; DB 11; Length 854;
 Best Local Similarity 100.0%; Pred. No. 3.3e-98;
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGGACCCCAAGCCTCAACCCCAAGACACAGCGGCTTATGTGCTGACTTTGTAGGCTAT 60
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 196 ATGGGACCCCAAGCCTCAACCCCAAGACACAGCGGCTTATGTGCTGACTTTGTAGGCTAT 255
 |||||
 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120
 |||||
 256 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 315
 |||||
 121 CCGCTGACCAAGCAGATGCGGGCTGCTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180
 |||||
 316 CCGCTGACCAAGCAGATGCGGGCTGCTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 375
 |||||
 181 TTCTGTACCTGCGCGCTGCTGACCTGACGTCAGCCCAAGGCTCAAGCAGTTCAC 240
 |||||
 376 TTCTGTACCTGCGCGCTGCTGACCTGACGTCAGCCCAAGGCTCAAGCAGTTCAC 435
 |||||
 241 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAAGTGGGGCCGCTTGTGCAATTTCTT 300
 |||||
 436 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAAGTGGGGCCGCTTGTGCAATTTCTT 495
 |||||
 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCITTTGTGGA 360
 |||||
 496 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCITTTGTGGA 555
 |||||
 361 CAAATGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGCTGACTGATTCACAGC 420
 |||||
 556 CAAATGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGCTGACTGATTCACAGC 615
 |||||
 421 AGTGGGGGCTGGG 433
 |||||
 616 AGTGGGGGCTGGG 628

RESULT 12

BC298789 792 bp mRNA linear EST 21-FEB-2001
 LOCUS 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',
 DEFINITION mRNA sequence.

ACCESSION BC298789
 VERSION BC298789.1 GI:13063794
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS NIH-MGC http://mgi.mgi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: The Cepo Laboratories, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov

Plate: L1AM10394 row: e column: 08
 High quality sequence stop: 713.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="IMAGE:4511215"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: pCMV-SORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 72.3%; Score 420.2; DB 12; Length 792;
 Best Local Similarity 99.1%; Pred. No. 5.4e-95;
 Matches 433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1 ATGGGACCCCAAGCCTCAACCCCAAGACACAGCGGCTTATGTGCTGACTTTGTAGGCTAT 60
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 99 ATGGGACCCCAAGCCTCAACCCCAAGACACAGCGGCTTATGTGCTGACTTTGTAGGCTAT 158
 |||||
 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120
 |||||
 159 AAGCTGAGGACAGAGGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 218
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 121 CCGCTGACCAAGCAGATGCGGGCTGCTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 180
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 219 CCGCTGACCAAGCAGATGCGGGCTGCTGAGAGAGAGTTTGAAGCCGTTTCCGCGCAC 278
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 181 TTCTGTACCTGCGCGCTGCTGACCTGACGTCAGCCCAAGGCTCAAGCAGTTCAC 240
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 279 TTCTGTACCTGCGCGCTGCTGACCTGACGTCAGCCCAAGGCTCAAGCAGTTCAC 337
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 241 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAAGTGGGGCCGCTTGTGCAATTTCTT 300
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 338 CAGGTTTCCGAGCACTTTTCCAGGGGGCCCTTAAGTGGGGCCGCTTGTGCAATTTCTT 397
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 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCITTTGTGGA 360
 |||||
 398 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCITTTGTGGA 457
 |||||
 361 CAAATGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGCTGACTGATTCACAGC 420
 |||||
 458 CAAATGACAGATTGATGTGTGCTTACTGTGAGACAGCTGTGCTGACTGATTCACAGC 517
 |||||
 421 AGTGGGGGCTGGG 437
 |||||
 518 AGTGGGGGCTGGTAA 534

RESULT 13

CB578463 623 bp mRNA linear EST 03-APR-2003
 LOCUS CB578463
 DEFINITION AMGNNUC:NRDGL-00100-H10-A nrdgl (10855) Rattus norvegicus cDNA
 clone nrdgl-00100-h10 5', mRNA sequence.

ACCESSION CB578463
 VERSION CB578463.1 GI:29522504
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS Amgen EST Program
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick

Amgen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00100 row: h column: 10.
Location/Qualifiers

FEATURES

source

1..623
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nr01-00100-110"
/issue="Dorsal Root Ganglia"
/clone_lib="nr01 (10855)"
/note="Vector: pSPOR1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"

ORIGIN

Query Match 72.0%; Score 418.6; DB 14; Length 623;
Best Local Similarity 97.9%; Pred. No. 1.2e-94;
Matches 424; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCAAGCTTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGCTAT 60
Db 191 ATGGGACCCCAAGCTTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGCTAT 250
Qy 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCAAGCCGCGAC 120
Db 251 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCCAAGCCGCGAC 310
Qy 121 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGACAGATTGAGACCCGTTCCGCGCAC 180
Db 311 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGACAGATTGAGACCCGTTCCGCGCAC 370
Qy 181 TTCTCTGACTGCGGCTGCTGAGTACAGTGAACCCAGGCTGAGCCCAAGCGTTCCAC 240
Db 371 TTCTCTGACTGCGGCTGCTGAGTACAGTGAACCCAGGCTGAGCCCAAGCGTTCCAC 430
Qy 241 CAGGTTCCGAGCACTTTTCCAGAGGGGCGCTTACGCGGCGCTGCTGAGCAATTCCTT 300
Db 431 CAGGTTCCGAGCACTTTTCCAGAGGGGCGCTTACGCGGCGCTGCTGAGCAATTCCTT 490
Qy 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Db 491 GTCTTTGGGGCTGCGCTGTGTGCTGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 550
Qy 361 CAAGTGAAGAGATTGATGTGTGCTGAGTGTGAGACAGCTGCTGCTGATGATCCAGC 420
Db 551 CAAGTGAAGAGATTGATGTGTGCTGAGTGTGAGACAGCTGCTGCTGATGATCCAGC 610
Qy 421 AGTGGGGGCTGGG 433
Db 611 AGTGGGGGCTGGG 623

RESULT 14
AM258810 540 bp mRNA linear EST 23-DEC-1999
LOCUS um74a02.y1 Sugano mouse kidney mRna Mus musculus cDNA clone
DEFINITION IMAGE:2300906 5' similar to SW:BCIM_MOUSE P70345 APOPTOSIS
REULATOR BCL-W. [2] SW:BCIM_MOUSE ; mRNA sequence.
ACCESSION AM258810
VERSION AM258810.1 GI:6631791
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muride; Murinae; Mus.
REFERENCE 1 (bases 1 to 540)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Peterson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuk,R.,
Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL COMMENT

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:1009678

FEATURES

source

Seg primer: custom primer used
High quality sequence stop: 465.
Location/Qualifiers

1..540
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2300906"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mRna"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGG); Site_2: DraIII (CACTGTGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTATTTTATTTT]; double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCTTACTGG), digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGG, 3' site CACCAATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGTGCTTAAAGCTGCG and 3' end
primer CGACTGACCTCGAGCACA."

ORIGIN

Query Match 71.4%; Score 414.8; DB 10; Length 540;
Best Local Similarity 99.3%; Pred. No. 1e-93;
Matches 427; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 ATGGGACCCCAAGCTTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGGCTAT 60
Db 112 ATGGGACCCCAAGCTTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGGCTAT 171
Qy 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 120
Db 172 AAGCTGAGGAGGAGGTTATGTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 231
Qy 121 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGACAGATTGAGACCCGTTTCCGCGCAC 180
Db 232 CCGCTGCACCAAGCCATGCGGCTGCTGAGAGACAGATTGAGACCCGTTTCCGCGCAC 291
Qy 181 TTCTCTGACTGCGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 240
Db 292 TTCTCTGACTGCGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 351
Qy 241 CAGGTTCCGAGCACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTCTTGGGCAATTCCTT 300
Db 352 CAGGTTCCGAGCACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTCTTGGGCAATTCCTT 411
Qy 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Db 412 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 471
Qy 361 CAAGTGAAGAGATTGATGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 420
Db 472 CAAGTGAAGAGATTGATGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 530
Qy 421 AGTGGGGGCT 430
Db 531 AGTGGGGGCT 540

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:06:41; Search time 60 Seconds
(without alignments)
908.861 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009
Sequence: 1 MATPASTPDRALVADRVGY.....LTGAVALGALVTGAFRASK 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

1: Geneseqp19808: *
2: Geneseqp19908: *
3: Geneseqp20008: *
4: Geneseqp20018: *
5: Geneseqp20028: *
6: Geneseqp20038: *
7: Geneseqp20048: *
8: Geneseqp20058: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1009	100.0	193	2	AAV05531 Mouse Bcl
2	1005	99.6	193	2	AAW61391 Rat bcl-y
3	1005	99.6	193	2	AAW97391 The rat b
4	1000	99.1	192	2	AAW97393 Protein s
5	1000	99.1	193	2	AAV05530 Human Bcl
6	1000	99.1	193	7	ADDA6742 Human Pro
7	995	98.6	193	2	AAW61392 Human bcl
8	995	98.6	193	2	AAW97392 The human
9	993	98.4	193	2	AAW36047 Human bcl
10	993	98.4	193	2	AAV05532 Human Bcl
11	990	98.1	192	2	AAW97394 Mammalian
12	967.5	95.9	192	2	AAV05533 Mouse Bcl
13	876	86.8	168	2	AAW36048 Mouse bcl
14	814.5	80.7	190	5	AAO18223 Human Bcl
15	759	75.2	365	2	AAW59884 Amino aci
16	759	75.2	365	5	ABG95556 Human nov
17	759	75.2	365	6	ABO34750 Fragment
18	432.5	42.9	411	5	AAU00219 Bcl-XL-DT
19	430.5	42.7	237	5	ABG78480 Wild type
20	428.5	42.5	233	4	AAW73303 Rat wild-
21	428.5	42.5	233	7	ADBE62921 Rat Prote
22	428.5	42.4	233	7	ADBE62921 Rat Prote
23	427.5	42.4	233	2	AAW68887 Human thy
24	427.5	42.4	233	2	AAW05821 Bcl-XL pr
25	427.5	42.4	233	2	AAW31530 Human ant

26	427.5	42.4	233	3	AAV69969 Human Bcl
27	427.5	42.4	233	3	AAW83223 Bcl-x pol
28	427.5	42.4	233	4	AAW50538 Human Bcl
29	427.5	42.4	233	4	AAW64262 Human Bcl
30	427.5	42.4	233	4	AAW47515 Protein e
31	427.5	42.4	233	7	ADBE62493 Human Pro
32	427.5	42.4	236	6	ABR83558 To1A-BCL
33	427.5	42.4	348	6	ABR83557 To1A-BCL
34	425	42.1	225	2	AAW19396 "Depreryl
35	424.5	42.1	233	4	AAW73304 Mutant ra
36	415.5	41.2	239	4	AAW64037 Human Bcl
37	414.5	41.1	152	6	AAW79760 Bcl-XL. 4
38	412	40.8	236	4	AAW35131 Murine Bc
39	412	40.8	236	5	AAW76554 Murine Bc
40	411.5	40.8	239	2	AAW87810 A human B
41	411.5	40.8	239	4	AAW35130 Human Bcl
42	411.5	40.8	239	4	AAW74127 Human bcl
43	411.5	40.8	239	5	ABG78479 Human Bcl
44	411.5	40.8	239	5	ABG78478 Human Bcl
45	411.5	40.8	239	5	AAW76553 Human Bcl

ALIGNMENTS

RESULT 1	AAV05531	standard; protein; 193 AA.
ID	AAV05531	
XX	AAV05531	
AC	AAV05531	
DT	05-JUL-1999	(first entry)
XX		
DE	Mouse Bcl-w protein essential for spermatogenesis.	
XX		
KW	Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility; animal model.	
KM		
XX		
OS	Mus sp.	
XX		
PN	W09913710-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998;	98WO-AU000764.
XX		
PR	16-SEP-1997;	97AU-00009228.
XX		
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
XX		
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F,	
XX		
DR	WPI: 1999-243890/20.	
XX		
PT	N-FSDB; AAX25133.	
XX		
PS	An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.	
XX		
PS	Claim 2; Page 35; 52pp; English.	
XX		
CC	The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals.	
CC	Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene (see AAX25133-35) or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise	

CC Facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 1009; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPGPADPLHQMRRAAGDEFETRRFRT 60
DB 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPGPADPLHQMRRAAGDEFETRRFRT 60
QY 61 FSDLAQLHVTGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
QY 121 QVODMMVAYLETRLADWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
DB 121 QVODMMVAYLETRLADWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 2

ID AAM61391 standard; protein; 193 AA.

XX AAM61391;
AC 02-OCT-1998 (first entry)
DT Rat bcl-y protein.
DE bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
KW Rattus sp.
OS
XX US5789201-A.
XX
XX 04-AUG-1998.
XX
XX 11-FEB-1997; 97US-00798897.
XX
XX 23-FEB-1996; 96US-0012201P.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI, 1998-446079/38.
XX
XX N-PSDB; AAV28333.
XX
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
XX recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX
XX Example; Fig 3A; 27pp; English.

CC The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired

XX Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 2e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPGPADPLHQMRRAAGDEFETRRFRT 60
DB 1 MATPASTPTRALVADPFVGYKLRQKGYVCGAGPGGPGPADPLHQMRRAAGDEFETRRFRT 60
QY 61 FSDLAQLHVTGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQOQRTQVSDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
QY 121 QVODMMVAYLETRLADWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
DB 121 QVODMMVAYLETRLADWIIHSSGMAEFTALYGDGALBEARLRREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 3

ID AAM97391 standard; protein; 193 AA.

XX AAM97391;
AC 20-MAY-1999 (first entry)
DT The rat bcl-y protein.
DE
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

OS Rattus sp.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-00978523.
XX
XX 23-FEB-1996; 96US-0012201P.
XX
XX 11-FEB-1997; 97US-00798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI, 1999-214150/18.
XX
XX N-PSDB; AAX15945.
XX
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX
XX Disclosure; Col 15-18; 26pp; English.

CC The present sequence represents rat bcl-y protein (Rbcl-y). The
XX specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended

period. In contrast, if they act as cell death stimulators, Bcl-Y and Hbcl-Y may be used to treat conditions associated with prolonged cell life span such as cancer (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites

Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;

Best Local Similarity 99.5%; Pred. No. 2e-101; Mismatches 1; Indels 0; Gaps 0;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFERFRRTF 60

DB 1 MATPASTPDTALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFERFRRTF 60

QY 61 FSDLAOLHVTGPSAQGRFTQVSDLPFGGPNWGRVAFVFGALCAESVNKMEPLVG 120

DB 61 FSDLAOLHVTGPSAQGRFTQVSDLPFGGPNWGRVAFVFGALCAESVNKMEPLVG 120

QY 121 QVQDMVAVYLETRLADWTHSSGMAEFTALYGDGALBEARLRREGNMAVSRVTLTGAVAL 180

DB 121 QVQDMVAVYLETRLADWTHSSGMAEFTALYGDGALBEARLRREGNMAVSRVTLTGAVAL 180

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

DB 181 GALVTGAFPAK 193

QY 181 GALVTGAFPAK 193

with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Bcl-Y and Hbcl-Y may be used to treat conditions associated with prolonged cell life span such as cancer (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites

Sequence 192 AA;

Query Match 99.1%; Score 1000; DB 2; Length 192;

Best Local Similarity 99.5%; Pred. No. 7.1e-101; Mismatches 1; Indels 0; Gaps 0;

Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPDTALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFERFRRTF 61

DB 1 ATPASTPDTALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFERFRRTF 60

QY 62 SDLAOLHVTGPSAQGRFTQVSDLPFGGPNWGRVAFVFGALCAESVNKMEPLVG 121

DB 61 SDLAOLHVTGPSAQGRFTQVSDLPFGGPNWGRVAFVFGALCAESVNKMEPLVG 120

QY 122 QVQDMVAVYLETRLADWTHSSGMAEFTALYGDGALBEARLRREGNMAVSRVTLTGAVAL 181

DB 121 QVQDMVAVYLETRLADWTHSSGMAEFTALYGDGALBEARLRREGNMAVSRVTLTGAVAL 180

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

DB 181 ALVTGAFPAK 192

QY 182 ALVTGAFPAK 193

RESULT 5

AA05530

ID AA05530 standard; protein; 193 AA.

AC AA05530;

DT 05-JUL-1999 (first entry)

DE Human Bcl-w protein essential for spermatogenesis.

OS Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;

PN animal model.

PN Homo sapiens.

PN MO9913710-A1.

PN 25-MAR-1999.

PN 16-SEP-1998;

PN 98WO-AU000764.

PN 16-SEP-1997;

PN 97AU-00009228.

PN (HALL-) HALL INST MEDICAL RES WALTER & ELITA.

PN Cory S, Adams J, Print C, Gibson L, Koentgen F;

PN WPI; 1999-243890/20.

PN N-PSDB; AAX25132.

PN An animal model exhibiting reduced levels of a Bcl-w protein and/or

PN protein associated with Bcl-w.

PN Claim 2; Page 33; 52pp; English.

PN The present sequence is human Bcl-w, a pro-survival member of the Bcl-2

CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation in at least one allele of the human or murine bcl-w gene (see
CC AX2512-35) or in a gene associated with bcl-w. Such animals have
CC disorganized seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
CC
XX SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYCGAGPGGPGADPLHQMRAGDEFETRRPT 60
DB 1 MATPASAPDTRALVADPFVGYKLRQKGYCGAGPGGPGADPLHQMRAGDEFETRRPT 60
QY 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
QY 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARRLRBGNMWSVRTVLGAVALL 180
DB 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARRLRBGNMWSVRTVLGAVALL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 6
ADD46742
ID ADD46742 standard; protein; 193 AA.

XX ADD46742;
AC 29-JAN-2004 (first entry)
DT Human Protein Q92843, SEQ ID NO 12427.
XX DE Human
XX KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNF; Chung.
XX OS Homo sapiens.
OS WO2003016475-A2.
PN 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
PF 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; Q92843.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page: 1017pp; English.

PS The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 7; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYCGAGPGGPGADPLHQMRAGDEFETRRPT 60
DB 1 MATPASAPDTRALVADPFVGYKLRQKGYCGAGPGGPGADPLHQMRAGDEFETRRPT 60
QY 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDDELFOGPGNMGRLVAFVFGAALCAESVKNKEPVLVG 120
QY 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARRLRBGNMWSVRTVLGAVALL 180
DB 121 QVQDMVMVAYLETRLDWTHSSGMAEFTALYGDGALBEARRLRBGNMWSVRTVLGAVALL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 7
AAM61392
ID AAM61392 standard; protein; 193 AA.

XX AAM61392;
AC 02-OCT-1998 (first entry)
DT Human bcl-y protein.
XX DE Human bcl-y protein.
XX KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX OS Homo sapiens.
OS US5789201-A.
PN 04-AUG-1998.
PD 11-FEB-1997; 97US-00798897.
XX

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XX 23-FEB-1996; 96US-0012201P.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI; 1998-446079/38.
XX N-PSDB; AAV28334.
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX Example; Column 17/18; 27pp; English.
XX The mammalian bcl-1 protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-1 falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired
XX
XX Sequence 193 AA;
SQ
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADFGYGLRQKGYVCGAPGEGPAADPLHOAMRAAGDEFETRRPRT 60
Db 1 MATPASAPDTRALVEDFGYGLRQKGYVCGAPGEGPAADPLHOAMRAAGDEFETRRPRT 60
QY 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
Db 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
Db 121 QVQDMWVAYLETRLADWIIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
QY 181 GALVTGAFPFASK 193
Db 181 GALVTGAFPFASK 193
RESULT 8
AAW97392 standard; protein; 193 AA.
XX AAW97392;
XX 20-MAY-1999 (first entry)
XX The human bcl-1 protein.
XX
XX Rat bcl-1 protein; Rbcl-1; human bcl-1 protein; Hbcl-1; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
XX Homo sapiens.
XX US5883229-A.
XX 16-MAR-1999.
XX 25-NOV-1997; 97US-00978523.

```

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XX 23-FEB-1996; 96US-0012201P.
XX 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI; 1999-214150/18.
XX N-PSDB; AAX15946.
XX Novel bcl-1 homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX Claim 1; Col 17-18; 26pp; English.
XX
XX The present sequence represents human bcl-1 protein (Hbcl-1). The
XX specification also describes rat bcl-1 protein (Rbcl-1). Rbcl-1 and Hbcl-
XX Y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-1 and Hbcl-1
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-1 and
XX Hbcl-1 may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites
XX
XX Sequence 193 AA;
SQ
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADFGYGLRQKGYVCGAPGEGPAADPLHOAMRAAGDEFETRRPRT 60
Db 1 MATPASAPDTRALVEDFGYGLRQKGYVCGAPGEGPAADPLHOAMRAAGDEFETRRPRT 60
QY 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
Db 61 FSDLAQLHVTTPGSAQGRFTQVSDLEFGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWIIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
Db 121 QVQDMWVAYLETRLADWIIHSSGWAFFETALYGDGALBEARLRGNNASVETVLTGAVAL 180
QY 181 GALVTGAFPFASK 193
Db 181 GALVTGAFPFASK 193
RESULT 9
AAW36047 standard; protein; 193 AA.
XX AAW36047;
XX 22-APR-1998 (first entry)
XX Human bcl-1 protein.
XX
XX Bcl-1; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease.
XX Homo sapiens.

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PN W09735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP,
XX
DR WPI; 1997-489635/45.
XX
N-PSDB; AAT96577.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
XX
PS diseases.
XX
PS Claim 6; Page 48; 86pp; English.
XX
CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
XX
CC -2 gene family and extracted from an adult brain library. This gene
XX
CC promotes cell survival, so its modulation is useful in treatment of
XX
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
XX
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
XX
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
XX
CC Up-regulation of the gene can also be used to modify cell lines cultured
XX
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
XX
CC and to increase survival of primary explants during genetic modification.
XX
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
XX
CC antibody production or screening of potential modulators
XX
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
Best Local Similarity 97.9%; Pred. No. 4.2e-100;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFERFRRT 60
DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFERFRRT 60
QY 61 FSDLAOLHVTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120
DB 61 FSDLAOLHVTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMASVRTLGAVAL 180
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 10
AAV05532
ID AAV05532 standard; protein; 193 AA.
XX
AC AAV05532;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
XX
KW animal model.
XX
OS Homo sapiens.
XX
PN W09913710-A1.

PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
XX
N-PSDB; AAX25134.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 37; 52pp; English.
XX
CC The present sequence is described of a derivative of human Bcl-w (see
XX
CC also AAV05530), a pro-survival member of the Bcl-2 family that is widely
XX
CC expressed and which is essential for spermatogenesis. The invention
XX
CC relates generally to a method of treatment and to an animal model for the
XX
CC identification of molecules and genetic sequences useful for inducing or
XX
CC reducing fertility of male animals. Methods are provided for the
XX
CC treatment of infertility, or for reducing fertility, by modulating
XX
CC spermatogenesis. An animal model carries a mutation is at least one
XX
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
XX
CC associated with bcl-w. Such animals have disorganised seminiferous tubules
XX
CC and are substantially infertile, but possess no other major abnormalities
XX
CC as determined by histological examination. They can be used to screen for
XX
CC therapeutic molecules including genetic sequences capable of inducing,
XX
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
XX
CC can induce infertility
XX
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
Best Local Similarity 97.9%; Pred. No. 4.2e-100;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFERFRRT 60
DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFERFRRT 60
QY 61 FSDLAOLHVTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120
DB 61 FSDLAOLHVTGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEPVLG 120
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMASVRTLGAVAL 180
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALLEEARRLREGNMASVRTLGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 11
AAW97394
ID AAW97394 standard; protein; 192 AA.
XX
AC AAW97394;
XX
DT 20-MAY-1999 (first entry)
XX
DE Mammalian bcl-y protein.
XX
KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
XX
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX
KW premature cell death; cell death stimulator; prolonged cell life span;

KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 XX Mammalia.
 OS US5883229-A.
 XX 16-MAR-1999.
 PD 25-NOV-1997; 97US-00978523.
 XX 23-FEB-1996; 96US-0012201P.
 PR 11-FEB-1997; 97US-00798897.
 XX (COCE-) COCENSYS INC.
 PA Guastella J;
 PI WPI; 1999-214150/18.
 DR Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 XX modulating programmed cell death.
 PT
 PS Claim 2; Col 19-22; 26pp; English.
 XX
 CC The present sequence represents a mammalian bcl-y protein. The
 CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites
 CC
 XX Sequence 192 AA:
 SQ
 Query Match 98.1%; Score 990; DB 2; Length 192;
 Best Local Similarity 98.4%; Pred. No. 8.8e-100;
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPPTRALVADFVGYKLRQKGYVCGAGPGEGRPADPLHQAAMRAAGDEFFETRRRTF 61
 DB 1 ATPASAPPTRALVDFVGYKLRQKGYVCGAGPGEGRPADPLHQAAMRAAGDEFFETRRRTF 60
 QY 62 SDLAQAQLHTVTPGSAQOQRTVOVSDELFOGGMKRLVAFVFGALCAESYNKMEPLVIG 121
 DB 61 SDLAQAQLHTVTPGSAQOQRTVOVSDELFOGGMKRLVAFVFGALCAESYNKMEPLVIG 120
 QY 122 VQDMVAVLETRLDADWIIHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 181
 DB 121 VQDMVAVLETRLDADWIIHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVALG 180
 QY 182 ALVTVGAFPAASK 193
 DB 181 ALVTVGAFPAASK 192

RESULT 12
 AAY05533
 ID AAY05533 standard; protein; 192 AA.
 AC AAY05533;
 XX
 DT 05-JUL-1999 (first entry)

XX Mouse Bcl-w protein derivative.
 DE
 XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 XX
 OS Mus sp.
 XX WO9913710-A1.
 XX 25-MAR-1999.
 PD 16-SEP-1998; 98WO-AU000764.
 PR 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI WPI; 1999-243890/20.
 DR N-PSDB; AAX25135.
 XX
 CC An animal model exhibiting reduced levels of a Bcl-w protein and/or
 CC protein associated with Bcl-w.
 PT
 PS Disclosure; Page 39; 52pp; English.
 XX
 CC The present sequence is described of a derivative of mouse Bcl-w (see
 CC also AAY05533), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The derivative
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 XX Sequence 192 AA:
 SQ
 Query Match 95.9%; Score 967.5; DB 2; Length 192;
 Best Local Similarity 95.9%; Pred. No. 2.5e-97;
 Matches 185; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 MATPASTPPTRALVADFVGYKLRQKGYVCGAGPGEGRPADPLHQAAMRAAGDEFFETRRRT 60
 DB 1 MPTASTPPTRALVADFVGYKLRQKGYVCGAGPGEGRPADPLHQAAMRAAGDEFFETRRRT 60
 QY 61 FSDLAQAQLHTVTPGSAQOQRTVOVSDELFOGGMKRLVAFVFGALCAESYNKMEPLVIG 120
 DB 61 FSDLAQAQLHTVTPGSAQOQRTVOVSDELFOGGMKRLVAFVFGALCAESYNKMEPLVIG 120
 QY 121 QVQDMVAVLETRLDADWIIHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVAL 180
 DB 121 QVQDMVAVLETRLDADWIIHSSGMAEFTALYGDGALBEARLRREGNMAVTRVLTGAVAL 179
 QY 181 GALVTVGAFPAASK 193
 DB 180 GALVTVGAFPAASK 192

RESULT 13
 AAW36048
 ID AAW36048 standard; protein; 168 AA.
 AC AAW36048;
 XX
 DT

[illegible]

KW	cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
KW	neurotropic; neuroprotective; antiParkinsonian; virocidic; antiinflammatory;
KM	immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
KM	Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
KM	graft versus host disease; autoimmune disease.
XX	
OS	Unidentified.
XX	
PN	WO200248353-A2.
PD	
XX	20-JUN-2002.
PF	
XX	12-DEC-2001; 2001WO-EP014597.
XX	
PR	12-DEC-2000; 2000DE-01061766.
PR	04-JAN-2001; 2001DE-01000280.
XX	
PA	(APOT-) APOTECH RES & DEV LTD.
XX	
PI	Tschopp J, Hofmann K;
XX	
DR	WPI; 2002-537627/57.
XX	
PT	New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and
PT	for identifying therapeutic modulators of Bcl-Rambo function.
XX	
PS	Disclosure; Fig 1; 61pp; German.
XX	
CC	The present invention provides the protein and coding sequences of the
CC	human Bcl-Rambo apoptotic transcription factor, particularly the BHO
CC	domain. The sequences are useful in the treatment of diseases caused by
CC	incorrectly regulated intracellular signal transduction, including
CC	cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's
CC	diseases), muscular dystrophy, viral infections (including human
CC	immunodeficiency virus), autoimmune disease, septic shock, graft versus
CC	host disease and acute hepatitis. The present sequence is a protein
CC	described in the exemplification of the invention
XX	
SQ	Sequence 190 AA;
Query Match	80.7%; Score 814.5; DB 5; Length 190;
Best Local Similarity	87.0%; Pred. No. 1.4e-80;
Matches 168; Conservative 1; Mismatches 21; Indels 3; Gaps 3;	
QY	1 MATPASTPTDTRALVADFYGYLRQKGYCGAPGEGPAPADLHQAMRAAGDEFFTRFRKT 60
DB	1 MATPASAPXTYAXYAD-XGYTLRQKGYNGAGPGGAPAD-XHQAAXRAAGXEFETRFRT 58
QY	61 FSDLAALQCHVTPGSAQORFTQVSDLPQGGPNMGRILVAFVFGAALCAESYNKEMEPLVG 120
DB	59 FSDLAALQCHVTPGSAQORFTQVSDLPFGAKPMGKXXAFFFGAAXCAESYNKEMEPLVG 118
QY	121 QVODMMVAVYLETRADMIHSSGGAFFATLGDGALBEARLRREGNMASVETVLTGAVAL 180
DB	119 QXQEXMAVYLETXLAX-IHSSGGAFFATLGDGALBEARLRREGNMASVETVLTGAVAL 177
QY	181 GALVTVGAFEPASK 193
DB	178 GALVTVGAFEPASK 190
RESULT 15	
AAWS59884	
ID	AAWS59884 standard; protein; 365 AA.
XX	
AC	AAWS59884;
XX	
DT	20-NOV-1998 (First entry)
XX	
DE	Amino acid sequence of the cDNA clone Bcl-1ike (HAICH29).
XX	
KM	Bcl-1like (HAICH29); chronic inflammatory disease; allergic reaction;
KM	immunological disorder; autoimmune disease; anti-infectious agent.

XX Homo sapiens.
 OS
 XX W09831800-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US000960.
 PF
 XX 21-JAN-1997; 97US-0034204P.
 PR 21-JAN-1997; 97US-0034205P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (AUCK-) AUCKLAND UNISERVICES LTD.
 XX
 FI Ni J, Rosen CA, Gentz RL, Feng P, Krissansen GW, Su JY;
 XX
 XX WPI; 1998-414099/35.
 DR N-PSDB; AAV41925.
 XX
 XX New isolated polynucleotides and encoded polypeptides - used to develop
 PT products for treating e.g. inflammatory diseases, infections,
 PT immunological disorders, autoimmune diseases, allergies or tumours.
 XX
 PS Claim 1; Fig 12A-12D; 120pp; English.
 XX
 CC This is the amino acid sequence of the cDNA clone Bcl-1-like (HAICH29),
 CC used in the method of the invention. The products of the clone can be
 CC used for treating conditions associated with abnormal expression of the
 CC polypeptides. They can be used for e.g. treating chronic inflammatory
 CC diseases, immunological disorders, autoimmune diseases, inflammatory
 CC diseases, various allergies, and as anti-infectious agents. The products
 CC can also be used for detection and diagnosis
 XX
 SQ Sequence 365 AA;

Query Match 75.2%; Score 759; DB 2; Length 365;
 Best Local Similarity 98.6%; Pred. No. 3.9e-74;
 Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQKGYVCGAGPGEPADPLHQMRAAGDEFETRRRT 60
 |||||
 Db 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGEPADPLHQMRAAGDEFETRRRT 60
 QY 61 FSDLAQLHVTGPSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNKEPIVG 120
 |||||
 Db 61 FSDLAQLHVTGPSAQORFTQVSDDELFOGSPNMGRLVAFVFGAALCAESVKNKEPIVG 120
 QY 121 QVODMVAVLETRLADWTHSSGW 144
 |||||
 Db 121 QVODEMVAVLETRLADWTHSSGW 144

Search completed: February 26, 2004, 11:13:02
 Job time : 64 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:11:52 ; Search time 23 Seconds

(without alignments)
433.209 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009
Sequence: 1 MATPASTPDRALVADFGVY.....LTGVALGALVTGAFPRASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.p.pip:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	99.6	193	1	US-08-798-897-3
2	1005	99.6	193	2	US-08-978-523-3
3	1000	99.1	192	1	US-08-798-897-5
4	1000	99.1	192	2	US-08-978-523-5
5	995	98.6	193	1	US-08-798-897-4
6	995	98.6	193	2	US-08-978-523-4
7	990	98.1	192	1	US-08-798-897-6
8	990	98.1	192	2	US-08-978-523-6
9	759	75.2	365	4	US-09-148-476-696
10	759	75.2	365	4	US-09-010-147B-24
11	428.5	42.5	233	4	US-09-271-014A-6
12	427.5	42.4	233	1	US-08-333-565-59
13	427.5	42.4	233	1	US-08-081-448-6
14	427.5	42.4	233	1	US-08-607-269-24
15	427.5	42.4	233	1	US-08-471-058-14
16	427.5	42.4	233	2	US-08-661-479-59
17	427.5	42.4	233	2	US-08-470-670A-7
18	427.5	42.4	233	3	US-08-471-057-14
19	427.5	42.4	233	3	US-08-481-739-2
20	427.5	42.4	233	3	US-09-167-921-2
21	427.5	42.4	233	3	US-09-323-743-2
22	427.5	42.4	233	4	US-08-461-511A-7
23	427.5	42.4	233	4	US-08-470-865-14
24	427.5	42.4	233	5	PCT-US94-07089-7
25	427.5	42.4	233	5	PCT-US95-04600-24
26	425	42.1	225	3	US-09-101-519-1
27	423.5	42.0	233	1	US-08-607-269-23

28	423.5	42.0	233	5	PCT-US95-04600-23	Sequence 23, Appl
29	412	40.8	236	1	US-08-607-269-22	Sequence 22, Appl
30	412	40.8	236	5	US-09-127-048-9	Sequence 9, Appl
31	412	40.8	236	5	PCT-US95-04600-22	Sequence 22, Appl
32	411.5	40.8	239	1	US-08-112-208C-10	Sequence 10, Appl
33	411.5	40.8	239	1	US-08-248-819A-10	Sequence 10, Appl
34	411.5	40.8	239	2	US-08-337-646A-10	Sequence 10, Appl
35	411.5	40.8	239	2	US-08-856-531-10	Sequence 10, Appl
36	411.5	40.8	239	2	US-08-856-034-10	Sequence 10, Appl
37	411.5	40.8	239	3	US-09-127-048-8	Sequence 8, Appl
38	411.5	40.8	239	3	US-08-927-326-10	Sequence 10, Appl
39	411.5	40.8	239	4	US-09-379-820A-10	Sequence 10, Appl
40	409.5	40.6	239	1	US-08-333-565-51	Sequence 51, Appl
41	409.5	40.6	239	1	US-08-248-819A-12	Sequence 12, Appl
42	409.5	40.6	239	1	US-08-607-269-20	Sequence 20, Appl
43	409.5	40.6	239	1	US-08-471-058-12	Sequence 12, Appl
44	409.5	40.6	239	1	US-08-690-095-4	Sequence 4, Appl
45	409.5	40.6	239	2	US-08-465-485A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-3
Sequence 3, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gaestella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-3
Query Match 99.6%; Score 1005; DB 1; Length 193;
Best Local Similarity 99.5%; Pred. No. 5.9e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPDRALVADFGVYKLRQGYVCGAPGEGPAADBLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASTPDRALVADFGVYKLRQGYVCGAPGEGPAADBLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAALQHLTPGSAQQRFTVOVSDLEFQGGPMGRALVAFVFGAALCAESVKNEMPELVG 120

Db 61 FSDLAQLHVTGSGAQQRTQVSDLEFQGGPNMGRVAVFVGALCAESVKNKEPVLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 180
Db 121 QVQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 180
QY 181 GALVTGAFPAK 193
Db 181 GALVTGAFPAK 193

RESULT 2
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-3

Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 5.9e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPSTPTPRALVADVFVGKLRQKGYVCGAGGEGPADPLHQNRAGDEPFRFRRT 60
Db 1 MATPSTPTPRALVADVFVGKLRQKGYVCGAGGEGPADPLHQNRAGDEPFRFRRT 60
QY 61 FSDLAQLHVTGSGAQQRTQVSDLEFQGGPNMGRVAVFVGALCAESVKNKEPVLVG 120
Db 61 FSDLAQLHVTGSGAQQRTQVSDLEFQGGPNMGRVAVFVGALCAESVKNKEPVLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 180
Db 121 QVQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 180

QY 181 GALVTGAFPAK 193
Db 181 GALVTGAFPAK 193

RESULT 3
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-5

Query Match 99.1%; Score 1000; DB 1; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.2e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPTPRALVADVFVGKLRQKGYVCGAGGEGPADPLHQNRAGDEPFRFRRT 61
Db 1 ATPASTPTPRALVADVFVGKLRQKGYVCGAGGEGPADPLHQNRAGDEPFRFRRT 60
QY 62 SDLAQLHVTGSGAQQRTQVSDLEFQGGPNMGRVAVFVGALCAESVKNKEPVLVG 121
Db 61 SDLAQLHVTGSGAQQRTQVSDLEFQGGPNMGRVAVFVGALCAESVKNKEPVLVG 120
QY 122 VQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 181
Db 121 VQDMWVAVLETRLADWIIHSSGMAEFYALYGDGALBEARRLREGWASVRYTLTGAVAL 180
QY 182 ALVTGAFPAK 193
Db 181 ALVTGAFPAK 193

RESULT 4
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-5

Query Match 99.1%; Score 1000; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.2e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRRRTF 61
DB 1 ATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRRRTF 60
QY 62 SDLAQLAHLVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKMEPLVQ 121
DB 61 SDLAQLAHLVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKMEPLVQ 120
QY 122 VQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALG 181
DB 121 VQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALG 180
QY 182 ALVTVGAFPPASK 193
DB 181 ALVTVGAFPPASK 192

RESULT 5
US-08-798-897-4
Sequence 4, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
MEDIUM TYPE: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-4

Query Match 98.6%; Score 995; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 8.3e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRRRT 60
DB 1 MATPASTPDTRALVADPFVGYKLRQKGYVCGAGPGEGBPADPLHQAAMRAAGDEFETRRRT 60
QY 61 FSDLAQLAHLVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKMEPLVQ 120
DB 61 FSDLAQLAHLVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKMEPLVQ 120
QY 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVAL 180
DB 121 QVQDMVAVYLETRLADWIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVAL 180
QY 181 GALVTVGAFPPASK 193
DB 181 GALVTVGAFPPASK 192

RESULT 6
US-08-978-523-4
Sequence 4, Application US/0878523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
MEDIUM TYPE: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-523-4

Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 8.3e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPVGYKLRQKGYVCGAGPGEGPADPLHQMRAGDEFEFRFRRT 60
DB 1 MATPASAPDTRALVEDPVGYKLRQKGYVCGAGPGEGPADPLHQMRAGDEFEFRFRRT 60

QY 61 FSDLAQLHVTGSAQQRFTQVSDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120

QY 121 QVDMWVAVLETRLDWIMHSSGMAEFTLYDGALEEARRLREGNMAVRYTLTGAVALG 180
DB 121 QVDMWVAVLETRLDWIMHSSGMAEFTLYDGALEEARRLREGNMAVRYTLTGAVALG 180

QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 7
US-08-798-897-6
Sequence 6, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-6

Query Match 98.1%; Score 990; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 3.1e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPTRALVADPVGYKLRQKGYVCGAGPGEGPADPLHQMRAGDEFEFRFRRT 61
DB 1 ATPASAPDTRALVEDPVGYKLRQKGYVCGAGPGEGPADPLHQMRAGDEFEFRFRRT 60

QY 62 SDLAQLHVTGSAQQRFTQVSDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 121
DB 61 SDLAQLHVTGSAQQRFTQVSDELFOGPGPMWGRVAFVFGAALCAESVKNKEPVLVG 120

QY 122 QVDMWVAVLETRLDWIMHSSGMAEFTLYDGALEEARRLREGNMAVRYTLTGAVALG 181
DB 121 QVDMWVAVLETRLDWIMHSSGMAEFTLYDGALEEARRLREGNMAVRYTLTGAVALG 180

QY 182 ALVTGAFPAK 193
DB 181 ALVTGAFPAK 192

RESULT 8
US-08-978-523-6
Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-978-523-6

Query Match 98.1%; Score 990; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 3,1e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPSTEDTALVADPFVGYKLRQKGYCGAGPGEGPADPHQMRRAAGDEFFTRFRRTF 61
DB 1 ATPASADPTRALVDEDVFGYKLRQKGYCGAGPGEGPADPHQMRRAAGDEFFTRFRRTF 60

QY 62 SDLAQAQHVTPGSAQQRFTQVSDLFQCGPMMGRVAFVFPVGAALCAESVKNEMEPVVGQ 121
DB 61 SDLAQAQHVTPGSAQQRFTQVSDLFQCGPMMGRVAFVFPVGAALCAESVKNEMEPVVGQ 120

QY 122 VQDMVAVYLETRLADWHTSSGMAEFTALYGDGALBEARRLREGNMAVSRTLTGVAALG 181
DB 121 VQDMVAVYLETRLADWHTSSGMAEFTALYGDGALBEARRLREGNMAVSRTLTGVAALG 180

QY 182 ALVTVGAFPSAK 193
DB 181 ALVTVGAFPSAK 192

RESULT 9
US-09-149-476-696
Sequence 696; Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149, 476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040, 162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038, 621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047, 600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 618
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EARLIER APPLICATION NUMBER: 60/047, 503
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EARLIER APPLICATION NUMBER: 60/047, 592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 584

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056, 886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 879
EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 75.2% Score 759; DB 4; Length 365;
Best Local Similarity 98.6%; Pred. No. 2,1e-78;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFGYKLRQGYVCGAPGEPADPLHQMRAAGDEFTRFRRT 60
DB 1 MATPASAPDRALVADFGYKLRQGYVCGAPGEPADPLHQMRAAGDEFTRFRRT 60
QY 61 FSDLAQLHTVPGSAQCRFTQVSDELFGGNGWRLVAFVFGAALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVPGSAQCRFTQVSDELFGGNGWRLVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVQDMVAVLETRLDADWTHSSGW 144
DB 121 QVQDMVAVLETRLDADWTHSSGW 144

RESULT 10

US-09-010-147B-24
Sequence 24, Application US/09010147B

Patent No. 6653445

GENERAL INFORMATION:

APPLICANT: NI et al.

TITLE OF INVENTION: Human Proteins

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,147B

FILING DATE: 12-NO. 6653445-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,205

FILING DATE: 21-JAN-1997

APPLICATION NUMBER: US 60/034,204

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Jonathan L. Klein

REGISTRATION NUMBER: 41,119

REFERENCE/DOCKET NUMBER: PF353

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-010-147B-24
Query Match 75.2% Score 759; DB 4; Length 365;
Best Local Similarity 98.6%; Pred. No. 2,1e-78;

Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADFPVGYLROKGYCCGPGEGPAADPLHQMRAAGDEFETRRRT 60
 DB 1 MATPASAADTRALVADFPVGYLROKGYCCGPGEGPAADPLHQMRAAGDEFETRRRT 60

QY 61 FSDLAOLHTVTPGSAOORFTVSDLEFCGGPNMRLVAFVFGAALCAESVKNKMEPLVG 120
 DB 61 FSDLAOLHTVTPGSAOORFTVSDLEFCGGPNMRLVAFVFGAALCAESVKNKMEPLVG 120

QY 121 QVQDMVAVYLETTRLADWIHSSGGW 144
 DB 121 QVQDMVAVYLETTRLADWIHSSGGW 144

RESULT 11
 US-09-271-014A-6
 Sequence 6, Application US/09271014A
 Patent No. 6395510
 GENERAL INFORMATION:
 APPLICANT: THOMPSON, CRAIG B.
 TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
 FILE REFERENCE: ARCD:316
 CURRENT APPLICATION NUMBER: US/09/271.014A
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 6
 LENGTH: 233
 TYPE: PR1
 ORGANISM: Human
 US-09-271-014A-6

Query Match 42.5%; Score 428.5; DB 4; Length 233;
 Best Local Similarity 41.1%; Pred. No. 7.3e-41;
 Matches 92; Conservative 23; Mismatches 58; Indels 51; Gaps 4;

QY 11 RALVADFVGYLROKGYC-----GAGP-----GEGPAA 39
 DB 6 RELVADFVGYLROKGYC-----GAGP-----GEGPAA 39

QY 40 D-----PLHQMRAAGDEFETRRRTFSDLAOLHTVTPGSAOORFTQ 81
 DB 66 NGATPASHSSLDAREVIMPAVKQALREAGDEFELRYRRASFSDLTSQLHTPTGTAYQSFEQ 125

QY 82 VSDLEFCGGPNMRLVAFVFGAALCAESVKNKMEPLVGVQVQDMVAVYLETTRLADWIHSS 141
 DB 126 VVNLFFRDGVNMGRIVAFVFGAALCAESVKNKMEPLVGVQVQDMVAVYLETTRLADWIHSS 185

QY 142 GMAEFTALYDGALEEARLRE--GNWASVTVLTGAVAGAL 183
 DB 186 GMDTFLVLYGNNAALAESRKQGERFNRFLTGTMTVAGVLLGSL 229

RESULT 12
 US-08-333-565-59
 Sequence 59, Application US/08333565
 Patent No. 5622852
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
 TITLE OF INVENTION: REGULATOR
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,565
 FILING DATE: 31-OCT-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000700
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-333-565-59

Query Match 42.4%; Score 427.5; DB 1; Length 233;
 Best Local Similarity 41.3%; Pred. No. 9.6e-41;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYLROKGY-----V 28
 DB 6 RELVADFVGYLROKGY-----V 28

QY 29 CGAGPGEPAAD-----PLHQMRAAGDEFETRRRTFSDLAOLHTVTPGSAOORFT 80
 DB 66 NGA-TGHSSSLDAREVIMPAVKQALREAGDEFELRYRRASFSDLTSQLHTPTGTAYQSFE 124

QY 81 QVSDLEFCGGPNMRLVAFVFGAALCAESVKNKMEPLVGVQVQDMVAVYLETTRLADWIHSS 140
 DB 125 QVNLFFRDGVNMGRIVAFVFGAALCAESVKNKMEPLVGVQVQDMVAVYLETTRLADWIHSS 184

QY 141 SGMAEFTALYDGALEEARLRE--GNWASVTVLTGAVAGAL 183
 DB 185 NGMDTFLVLYGNNAALAESRKQGERFNRFLTGTMTVAGVLLGSL 229

RESULT 13
 US-08-081-448-6
 Sequence 6, Application US/08081448
 Patent No. 5646008
 GENERAL INFORMATION:
 APPLICANT: Thompson, Craig B.
 TITLE OF INVENTION: Vertebrate Apoptosis Gene:
 TITLE OF INVENTION: Compositions and Methods
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5646008th Clark Street, Suite 800
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,448
 FILING DATE: 19930622
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5646008thrup, Thomas E.
 REGISTRATION NUMBER: 33,268

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; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-081-448-6

Query Match 42.4%; Score 427.5; DB 1; Length 233;
Beeb Local Similarity 40.6%; Pred. No. 9, 6e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4

QY 11 RALVADPFGYKIRKRGY-----VCGAQP-----GEGCPA 39
D 6 RELVVDPLSTYKLSQKGSWSQSPDYVEENTTEAPGEGTESMETPPSALINGNPMSWHLASP 65
QY 40 D-----PLHQAPRAAGDEFETFRPRTFSDLAQLAHYTPGSAOORFTQ 81
D 66 NGATAHSSSLDAREYITPMAAVYQALREAGDEDELKRRKRFSDLTSGUHTTPGAYQSFQ 125
QY 82 VSDLFQGGPMMGRVLVAFVFGAALCAESVNMKEBLYGQVODMMVAYILETRIADMIHSS 141
D 126 VVNEFLPFDGVNMGRIYVAFPSFGALCVESVDKEMQVLVSRIAMMATYINDHLEPIQEN 185
QY 142 GGMAEFTALYGDGALAEARLAE--GNMASVRTVLTVGAVALGAL 183
D 186 GGMDFVELYGNMAAESRKQGERFNRMPLTGTNTAAGVLLDSL 229

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	US-08-607-269-24	TOPOLOGY: linear	
Query Match	42.4%	Score 427.5; DB 1;	Length 233;
Best Local Similarity	40.6%	Pred. No. 9.6e-41;	
Matches	91; Conservative	23; Mismatches	59; Indels 51; Gaps 4
Qy	11	RALVADFFGYLRLRKGY-----VCGAGP-----GEGPAA	39
Db	6	RELIVYDPLSTYLSLQKGYWSQSPDVEENRTAPRGTESEMEFPASLININPFWHLADSPAV	65
Qy	40	D-----PLHQMRAAGDEFFETRPRTESDLSAQLHVTGSAQOQRTQ	81
Db	66	NGATAHSSSLDAREVTPMAAAVKQALREAGDEFFELRYRRAFDLTLSOLHITPGTAQSPFQ	125
Qy	82	VSDLLFOGCGPWWGLVAFVFGALLCASVVKMEKPIVGOVQDMMVAALFETRLADWISS	141
Db	126	VVNELFRGVWGWGRIVAFSTFGALCVESVDKEMQVLSRLAAMATYTLNDHLEPFIQEN	185
Qy	142	GGMAEFTALYGDGALLEEARLRE--GNWASRTVLTGAVALGAL	183
Db	186	GGNLTFFVELLYGNMAAABSRKQGEFNNRFFLTGMVYAGVLLGSL	229

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1      RESULT 15
2      US-08-471-058-14
3      ; Sequence 14: Application US/08471058
4      ; Patent No. 5770443
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Kiefer, Michael C.
7      ; APPLICANT: Barr, Philip J.
8      ; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
9      ; TITLE OF INVENTION: PROTEIN, DNA ENCODING THE PROTEINS AND METHODS OF USE
10     ; TITLE OF INVENTION: THEREOF
11     ; NUMBER OF SEQUENCES: 24
12     ; CORRESPONDENCE ADDRESSES:
13     ; ADDRESSEE: MORRISON & FOERSTER
14     ; STREET: 755 PAGE MILL ROAD
15     ; CITY: Palo Alto
16     ; STATE: CA
17     ; COUNTRY: USA
18     ; ZIP: 94304-1018
19     ; COMPUTER READABLE FORM:
20     ; MEDIUM TYPE: Diskette
21     ; COMPUTER: IBM Compatible
22     ; OPERATING SYSTEM: DOS
23     ; SOFTWARE: FastSeq for Windows Version 2.0
24     ; CURRENT APPLICATION DATA:
25     ; APPLICATION NUMBER: US/08/471,058
26     ; FILING DATE: 06-JUN-1995
27     ; CLASSIFICATION: 800
28     ; PRIOR APPLICATION DATA:
29     ; APPLICATION NUMBER: 08/320,157
30     ; FILING DATE: 07-OCT-1994
31     ; APPLICATION NUMBER: 08/160,067
32     ; FILING DATE: 30-NOV-1993
33     ; ATTORNEY/AGENT INFORMATION:
34     ; NAME: lehnhardt, Susan K
35     ; REGISTRATION NUMBER: 33,943
36     ; REFERENCE/DOCKET NUMBER: 23647-20007.12
37     ; TELECOMMUNICATION INFORMATION:
38     ; TELEPHONE: 415-813-5600
39     ; TELEFAX: 415-494-0792
40     ; TELEX: 706141
41     ; INFORMATION FOR SEQ ID NO: 14:
42     ; SEQUENCE CHARACTERISTICS:
43     ; LENGTH: 233 amino acids
44     ; TYPE: amino acid
45     ; STRANDEDNESS: single
46     ; TOPOLOGY: linear
47     ;
48     ; US-08-471-058-14
49
50 Query Match          42.4%; Score 427.5; DB 1; Length 233;

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Best Local Similarity 41.3%; Pred. No. 9.6e-41;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

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Qy 11 RALVADFGYKLRQKY-----V 28
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Db 6 RELVVDPLSYKLSQGYGWSQPSDVEENRTEAPGCTESEMETPSAINGNPSMHLADSPAV 65
    |||:|||||
Qy 29 CGAGPGEGPAD-----PLHQMRAAGDEPFRFRRTFSDLAOLHTPGSAQQRFT 80
    |||:|||||
Db 66 NGA-TGHSSLDAREVTPMAAVKQALREAGDEFELETRRAPSDLTSLHTPGTRVQSFE 124
    |||:|||||
Qy 81 QVSDLEFGGPNMGRVLVAFVFGAALCAESVKNEMEPVGVQVODMVAYLETRLADWHS 140
    |||:|||||
Db 125 QVNNELFRDGVNKGRIVAFSFGALCVESVDKEMQVLVSRIAAAMATYLDHLEPWIGE 184
    |||:|||||
Qy 141 SGGWAFTALYGDGALREARLRE--GNWASRTVLTGAVALGAI 183
    |||:|||||
Db 185 NGGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVVLGSL 229
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Search completed: February 26, 2004, 11:15:37
Job time : 26 secs

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QY 181 GALVTVGAFPAK 193
Db 181 GALVTVGAFPAK 193

RESULT 2

US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US2002011943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

Query Match

Best Local Similarity 99.1%; Score 1000; DB 9; Length 193;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADPFVGYKLRQKGYCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGGRNMGRLVAFVFGALCAESVKNKEPVLVG 120
Db 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGGRNMGRLVAFVFGALCAESVKNKEPVLVG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180
Db 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180
QY 181 GALVTVGAFPAK 193
Db 181 GALVTVGAFPAK 193

RESULT 3

US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696

Query Match 75.2%; Score 759; DB 10; Length 365;
Best Local Similarity 98.6%; Pred. No. 5,7e-74;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFVGYKLRQKGYCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADPFVGYKLRQKGYCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60

QY 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGGRNMGRLVAFVFGALCAESVKNKEPVLVG 120
Db 61 FSDLAQLHVTTPGSAQOQRTQVSDELFOGGRNMGRLVAFVFGALCAESVKNKEPVLVG 120

QY 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180
Db 121 QVQDMWVAVLETRLDWIMHSSGMAEFTALYDGLAEARRLREGNMAVSRITVLGAVL 180

RESULT 4

US-09-882-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
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; PRIOR APPLICATION NUMBER: 60/047,583
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; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
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; PRIOR FILING DATE: 1997-05-23

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 PRIOR FILING DATE: 1997-04-11
 PRIOR APPLICATION NUMBER: 60/043,674
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 PRIOR FILING DATE: 1997-06-06
 PRIOR APPLICATION NUMBER: 60/056,886
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 PRIOR APPLICATION NUMBER: 60/056,636

PRIOR FILING DATE: 1997-08-22
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 PRIOR FILING DATE: 1997-08-22
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 PRIOR FILING DATE: 1997-05-23
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 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/048,964
 PRIOR FILING DATE: 1997-06-06
 PRIOR APPLICATION NUMBER: 60/057,650
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: 60/056,884
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/057,669
 PRIOR FILING DATE: 1997-09-05

Query Match 75.2%; Score 759; DB 10; Length 365;
 Best Local Similarity 98.6%; Pred. No. 5.7e-74;
 Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1  MATASPTDPTALVADPFVGYKLRQKGYCGAGPGBGPPADPLHOAMRAAGDEFETRPRRT 60
Db      1  MATPASADPTRALVADPFVGYKLRQKGYCGAGPGBGPPADPLHOAMRAAGDEFETRPRRT 60
Qy      61  FSDLAAGLHVTPGSAQGRFTQVSDLPFGCGPNMGRIVAFVFFGALCAESVNKMEPLVG 120
Db      61  FSDLAAGLHVTPGSAQGRFTQVSDLPFGCGPNMGRIVAFVFFGALCAESVNKMEPLVG 120
Qy      121  QVQDMVAVLETRLADWIHSSGGW 144
Db      121  QVQDMVAVLETRLADWIHSSGGW 144

RESULT 5
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to ger
; FILE REFERENCE: Case 1/1314
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-6

Query Match      45.3%; Score 457.5; DB 15; Length 179;
Best Local Similarity 52.0%; Pred. No. 1.4e-41;
Matches 91; Conservative 21; Mismatches 56; Indels 7; Gaps 2;

Qy      11  RALVADPFVGYKLRQKGYCGAGPGBGPPADPLHOAMRAAGDEFETRPRRTFSDLAAGLHV 70
Db      6  RELVADPFVGYKLRQKGYCGAGPGBGPPADPLHOAMRAAGDEFETRPRRTFSDLTSLHI 60
Qy      71  TPGSAQGRFTQVSDLPFGCGPNMGRIVAFVFFGALCAESVNKMEPLVGQVQDMVAVYL 130
Db      61  TPGTAYOSFEDEVVLELFRDGVNMGRIVAFVFFGALCAESVDKMOVYVSIASMAVLYL 120
Qy      131  ETRLADWIHSSGGAEFPTALYGDGALBEARLRLE--GNMASVTRVTLGCANVALGAL 183
Db      121  NDHLEPWTQDNQGMDFTEVELYGNNAAAESRQGRFRFRNWFPLTGMTVAGVALLGSL 175

RESULT 6
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to ger
; FILE REFERENCE: Case 1/1314
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del146-83)
US-10-402-017-8
Query Match 44.4%; Score 448.5; DB 15; Length 199;
Best Local Similarity 47.9%; Pred. No. 1,5e-40;
Matches 91; Conservative 21; Mismatches 61; Indels 17; Gaps 2;

OY 11 RALVADPVGYKLRQXGVC-----GAGPGCGPAADPLHQMRRAAGDEFET 55
D 6 RELVVDPLSYKLSQKGSWSQSPDVEENRTAEAGTESERAAAAAAVKQALREAGDEFEL 65
OY 56 RFRRTFSDLLAQLHVTPTGSAQORFTQVSDLPFGGPNWGRVLVAFVFGALCAESVKNEM 115
D 66 RYRAAFSDLSQHLITGTATYQSEFQGVNLEFRDGVNWRIVAFSFGALCVESVDKEM 125
OY 116 EPLVGQVQDMVAVYLETRLADWTHSSGGMAEFTALYGDGALBEARRLRE--GNWASVTV 173
D 126 QVLVSRIASWMAVTVLNDHLEPWIQDNGMDTFVELYGNNAASRKQGERFNNWFLTGMT 185
OY 174 LTGAVALGAL 183
D 186 VAGVLLGSL 195

RESULT 7
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEERTS and Martin FUSSENBERGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del166-83)
US-10-402-017-10
Query Match 43.8%; Score 441.5; DB 15; Length 219;
Best Local Similarity 43.3%; Pred. No. 1e-39;
Matches 91; Conservative 21; Mismatches 61; Indels 37; Gaps 2;

OY 11 RALVADPVGYKLRQXGVC-----CGAGPGE 35
D 6 RELVVDPLSYKLSQKGSWSQSPDVEENRTAEAGTESERETPSAINGNPSWMLADSPAV 65
OY 36 GPAADPLHQMRRAAGDEFETFRFRRTFSDLLAQLHVTPTGSAQORFTQVSDLPFGGPNWGR 95
D 66 AAAAAAVKQALREAGDEFELRYRAAFSDLSQHLITGTATYQSEFQGVNLEFRDGVNWR 125
OY 96 LVAFVFGALCAESVKNEMEPLVGQVQDMVAVYLETRLADWTHSSGGMAEFTALYGDGA 155
D 126 IVAFFSFGALCVESVDKEMQVLVSRIASWMAVTVLNDHLEPWIQDNGMDTFVELYGNNA 185
OY 156 LBEARRLRE--GNWASVTVLTGAVALGAL 183
D 186 AASRKQGERFNNWFLTGMTVAGVLLGSL 215

RESULT 8
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1

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GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12

Query Match 43.3%; Score 436.5; DB 15; Length 219;
Best Local Similarity 44.1%; Pred. No. 3.5e-39;
Matches 93; Conservative 22; Mismatches 57; Indels 39; Gaps 4;

Qy 11 RALVADFGYKLRKGY-----VCGAGPGECPAD-- 40
Db 6 RELVVDPLSTLSQKGYMSQPSDVEENRTAPEGTSEBRAAAANGA-TGHSSSLAR 64
Qy 41 -----PLHQARRAGDEFFETFRRTFSDLAOLHVTGSAQORFTQVSDLFQGGPNWG 94
Db 65 EVIPMAVKQALREAGDEFELRYRRAFSDLTSLHITGTAYQSEQVNNELFRDGVNMG 124
Qy 95 RLVAFFVFGALCAESVNKEMEPVVGQVDMVATLETRLADWIHSSGMAEFTLYGDG 154
Db 125 RIVAFSFGALCVESVDKEMQVLVSRJASWATYLDHLEPWIODNGMDTFVLYGN 184
Qy 155 ALEBARLRLE--GNVASRTVLTCGAVLAL 183
Db 185 AAESRKQGERPNRPFLLGTMTVAGVLLGSL 215

RESULT 9
US-10-402-017-4
; Sequence 4, Application US/10402017
; Publication No. US20030219671A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to get
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: *Cricetulus griseus*
US-10-402-017-4

Query Match 42.6%; Score 429.5; DB 15; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.2e-38;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

Qy 11 RALVADFGYKLRKGY-----V 28
Db 6 RELVVDPLSTLSQKGYMSQPSDVEENRTAPEGTSEBRTPSALINGNPSMHLADSPAV 65
Qy 29 CGAGPGECPAD-----PLHQARRAGDEFFETFRRTFSDLAOLHVTGSAQORFT 80
Db 66 NGA-TGHSSSLDAREVIMPAVKQALREAGDEFELRYRRAFSDLTSLHITGTAYQSPB 124

Qy 81 QVSDLEFQGGPNMGRVAFVFGAALCAESVNKEMEPVVGQVDMVATLETRLADWIHS 140
Db 125 QVNNELFRDGVNMGRIYAFSFGALCVESVDKEMQVLVSRJASWATYLDHLEPWIOD 184
Qy 141 SGMAEFTLYGDGALBARLRLE--GNVASRTVLTCGAVLAL 183
Db 185 GMDTFVLYGNNAAESRKQGERPNRPFLLGTMTVAGVLLGSL 229

RESULT 10
US-09-734-846-2
; Sequence 2, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingling
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-734-846-2

Query Match 42.4%; Score 427.5; DB 9; Length 233;
Best Local Similarity 40.6%; Pred. No. 3.6e-38;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Qy 11 RALVADFGYKLRKGY-----VCGAP-----GEGPAA 39
Db 6 RELVVDPLSTLSQKGYMSQPSDVEENRTAPEGTSEMETPSALINONPSMHLADSPAV 65
Qy 40 D-----PLHQARRAGDEFFETFRRTFSDLAOLHVTGSAQORFTQ 81
Db 66 NGATAHSSSLDAREVIMPAVKQALREAGDEFELRYRRAFSDLTSLHITGTAYQSPFQ 125
Qy 82 VSDLEFQGGPNMGRVAFVFGAALCAESVNKEMEPVVGQVDMVATLETRLADWIHS 141
Db 126 VNNELFRDGVNMGRIYAFSFGALCVESVDKEMQVLVSRJASWATYLDHLEPWIOD 185
Qy 142 GMAEFTLYGDGALBARLRLE--GNVASRTVLTCGAVLAL 183
Db 186 GMDTFVLYGNNAAESRKQGERPNRPFLLGTMTVAGVLLGSL 229

RESULT 11
US-09-952-278-6
; Sequence 6, Application US/09952278
; Patent No. US20020137182A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL

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?      COUNTRY: USA
?      ZIP: 60610
?
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: PatentIn Release #1.0, Version #1.25
?
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/09/952,718
?      FILING DATE: 12-Sep-2001
?      CLASSIFICATION: <Unknown>
?
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: US/08/081,448
?      FILING DATE: <Unknown>
?
?      ATTORNEY/AGENT INFORMATION:
?      NAME: NO. US20020137182althrup, Thomas E.
?      REGISTRATION NUMBER: 33,268
?      REFERENCE/DOCKET NUMBER: ARCD090
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 312-744-0090
?      TELEFAX: 312-755-4489
?
?      INFORMATION FOR SEQ ID NO: 6:
?
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 233 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?
?      MOLECULE TYPE: protein
?
?      SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

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[illegible]

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1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER: US/10/101,482
3      FILING DATE: 18-Mar-2002
4      CLASSIFICATION: <Unknown>
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US/08/320,157
7      FILING DATE: 07-OCT-1994
8      ATTORNEY/AGENT INFORMATION:
9      NAME: LEHNHARDT, SUSAN K.
10     REGISTRATION NUMBER: 33,943
11     REFERENCE/DOCKET NUMBER: 23647-20007.20
12     TELECOMMUNICATION INFORMATION:
13     TELEPHONE: (415) 813-5600
14     TELEFAX: (415) 494-0792
15     TELEX: 706141
16     INFORMATION FOR SEQ ID NO: 14:
17     SEQUENCE CHARACTERISTICS:
18     LENGTH: 233 amino acids
19     TYPE: amino acid
20     STRANDEDNESS: single
21     TOPOLOGY: linear
22     SEQUENCE DESCRIPTION: SEQ ID NO: 14:
23     US-10-101-482-14

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Query Match          42.4%; Score 427.5; DB 14; Length 233;
Best Local Similarity 41.3%; Pred. No. 3,6e-38;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4

Qy          11  RAIVADPVGYNLRQKGY-----V 28
Db          6  RELVVDLFLSYLXLSQKGYSSQFSDVEENRTPEAGTESEMETPSAINGNPSWHLADSPAV 65
Qy          29  CGAARPGEGPAD-----PLHQAMRAGDEFFRPRRTSDLAOLHVPNGSAQORFT 80
Db          66  NGA-TGSSSSLDABEVIPMAAVKQALRAGDEFLRYRRASDLTSQHLTPGTAYOSFE 124
Qy          81  QVSDLEFGCGENMGRILVAFVFGCALCAESYNKEMEPYGVGVODMVMVAYLETRLADWTHS 140
Db          125  QVNVLELRDGVGNMGRIVAFSFGGALCVESYDKENQVIVSNIIAAMATYINDHLEPWIOE 184
Qy          141  SGNAAEFTALYGDGALBEARRLRE--GNWASVRIVLYTCAVALGAL 183
Db          185  NGMDTFEVELYGNNAAAESRRGDERFNRWFLTGMTVAGVLLGSL 229

RESULT 13
US-10-072-830-4
: Sequence 4, Application US/10072830
: Publication No. US20030103945A1
: GENERAL INFORMATION:
: APPLICANT: CHEN, DONG FENG
: APPLICANT: HUANG, XIZHONG
: APPLICANT: CHEN, GUANG
: APPLICANT: MANJI, HUSSEINI K.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
: TITLE OF INVENTION: REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION
: FILE REFERENCE: ERM-105.01
: CURRENT APPLICATION NUMBER: US/10/072,830
: CURRENT FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: 60/267,832
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/272,617
: PRIOR FILING DATE: 2001-03-01
: PRIOR APPLICATION NUMBER: 60/289,990
: PRIOR FILING DATE: 2001-05-10
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 233
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-072-830-4

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Query Match 42.4%; Score 427.5; DB 14; Length 233;
 Best Local Similarity 40.6%; Pred. No. 3.6e-38;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFGYKLRQGY-----VCGAGP---GEGPAA 39
 DB 6 RELVADFLSYKLSQKGYSWGFSQFSDVENRTPEAGTSEMETPSAINGNPSMHLADSPAV 65
 QY 40 D-----PLHQMRRAAGDEFETRFRRTFSDDLAAQLHVTGSAQQRFTQ 81
 DB 66 NGATRAHSSSLDAREVIMPAAVKQALREAGDEFELRYRRAFSDLTSQHLITPGTAVQSFEQ 125
 QY 82 VSDELFOGQGNMGRVAFVFGAALCAESVKNKEPVLGVQVQVMVAVYLETRLADWIHSS 141
 DB 126 VVNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQEN 185
 QY 142 GGNAEFTALYGDGALBEARLR--GNWASVTVLTGAVLALGAL 183
 DB 186 GGMDFVELYGNNAASRKQGERFNRWFLTGMTVAGVLLGSL 229
 ; ORGANISM: Homo sapiens

RESULT 14

US-10-169-223-10
 ; Sequence 10, Application US/10169223
 ; Publication No. US20030152946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIMIZU, Shigeomi
 ; APPLICANT: TSUJIMOTO, Yoshihide
 ; TITLE OF INVENTION: BH4-Fused Polypeptides
 ; FILE REFERENCE: 1422-0537P
 ; CURRENT APPLICATION NUMBER: US/10/169, 223
 ; CURRENT FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: JP 11-371449
 ; PRIOR FILING DATE: 1999-12-27
 ; PRIOR APPLICATION NUMBER: PCT/JP00/09274
 ; PRIOR FILING DATE: 2000-12-26
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-169-223-10

Query Match 42.4%; Score 427.5; DB 14; Length 233;
 Best Local Similarity 40.6%; Pred. No. 3.6e-38;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFGYKLRQGY-----VCGAGP---GEGPAA 39
 DB 6 RELVADFLSYKLSQKGYSWGFSQFSDVENRTPEAGTSEMETPSAINGNPSMHLADSPAV 65
 QY 40 D-----PLHQMRRAAGDEFETRFRRTFSDDLAAQLHVTGSAQQRFTQ 81
 DB 66 NGATRAHSSSLDAREVIMPAAVKQALREAGDEFELRYRRAFSDLTSQHLITPGTAVQSFEQ 125
 QY 82 VSDELFOGQGNMGRVAFVFGAALCAESVKNKEPVLGVQVQVMVAVYLETRLADWIHSS 141
 DB 126 VVNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQEN 185
 QY 142 GGNAEFTALYGDGALBEARLR--GNWASVTVLTGAVLALGAL 183
 DB 186 GGMDFVELYGNNAASRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 15

US-10-302-262-2
 ; Sequence 2, Application US/10302262
 ; Publication No. US20030191300A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Montia, Brett P.

APPLICANT: Nickoloff, Brian J.
 APPLICANT: Zhang, Qiongling
 TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
 FILE REFERENCE: ISPH-0528
 CURRENT APPLICATION NUMBER: US/10/302,262
 CURRENT FILING DATE: 2002-11-21
 PRIOR APPLICATION NUMBER: US/09/734,846
 PRIOR FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: 09/277,020
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 09/167,921
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 09/323,743
 PRIOR FILING DATE: 1999-06-02
 NUMBER OF SEQ ID NOS: 74
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 233
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-302-262-2

Query Match 42.4%; Score 427.5; DB 14; Length 233;
 Best Local Similarity 40.6%; Pred. No. 3.6e-38;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFGYKLRQGY-----VCGAGP---GEGPAA 39
 DB 6 RELVADFLSYKLSQKGYSWGFSQFSDVENRTPEAGTSEMETPSAINGNPSMHLADSPAV 65
 QY 40 D-----PLHQMRRAAGDEFETRFRRTFSDDLAAQLHVTGSAQQRFTQ 81
 DB 66 NGATRAHSSSLDAREVIMPAAVKQALREAGDEFELRYRRAFSDLTSQHLITPGTAVQSFEQ 125
 QY 82 VSDELFOGQGNMGRVAFVFGAALCAESVKNKEPVLGVQVQVMVAVYLETRLADWIHSS 141
 DB 126 VVNELFRDGVNMGRIVAFSFGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQEN 185
 QY 142 GGNAEFTALYGDGALBEARLR--GNWASVTVLTGAVLALGAL 183
 DB 186 GGMDFVELYGNNAASRKQGERFNRWFLTGMTVAGVLLGSL 229

Search completed: February 26, 2004, 11:16:23
 Job time : 36 secs

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1	428.5	42.5	233	2	I49056	bcl-x-long - mouse
2	427.5	42.4	233	2	B47537	apoptosis regulator
3	424.5	42.1	233	2	S51761	BCL-X protein - rat
4	423.5	42.0	233	2	A37332	transforming prote
5	414	41.0	232	2	S24390	transforming prote
6	411.5	40.8	239	1	TVH0A1	transforming prote
7	411	40.7	236	2	I67432	BCL-2 - rat (Eragm
8	406	40.2	236	2	I53744	gene bcl-2 protein
9	405	40.1	236	1	TVMSA1	transforming prote
10	404.5	40.1	233	2	I67431	BCL-X-long - rat
11	402	39.8	236	2	UC7383	B-cell lymphoma 2
12	378	37.5	190	2	A47537	apoptosis regulator
13	377.5	37.4	214	2	I49057	bcl-x transmembran
14	374.5	37.1	227	1	JEO303	apoptosis regulato
15	356	35.3	216	2	B37332	transforming prote
16	348.5	34.5	199	1	TVMSB1	transforming prote
17	345	34.2	205	1	TVH0B1	transforming prote
18	277.5	27.5	154	2	I58194	gene bcl-2 protein
19	182	18.0	170	2	I49055	bcl-x-short - mous
20	174	17.2	176	2	I67435	gene bcl-xhort pr
21	171	16.9	211	2	S58873	Bak protein - huma
22	168	16.7	211	2	S58875	cdn-2 protein - hu
23	158.5	15.7	192	2	D47538	bcl-2-associated p
24	154	15.3	192	2	A47538	bcl-2-associated p
25	151	15.0	261	2	H88578	protein ced-9 (limp
26	151	15.0	280	2	A53189	apoptosis suppress
27	150.5	14.9	133	2	I53395	bcl-2-associated p
28	147.5	14.6	179	2	JC7355	Bax-delta protein
29	147.5	14.6	218	2	B47538	bcl-2-associated p

30	142	14.1	177	2	S54778	NR-13 protein - qu
31	138.5	13.7	143	2	I38921	bol-2-associated p
32	138	13.7	225	2	UC7567	Mc1-a protein - z
33	116	11.5	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47466	BCL2 homolog MCL1
35	105	10.4	172	2	I48449	hemopoietic-specif
36	88	8.7	155	2	B83217	hypothetical prote
37	87	8.6	3433	1	GNMVKV	genome polyprotein
38	86.5	8.6	301	2	T36534	probable lipase/es
39	86	8.5	270	2	A12598	dihydrodipicolinat
40	85	8.5	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	378	1	AJLCO8	glutamate-ammonia
42	83.5	8.3	872	2	G98026	alanine-tRNA ligas
43	83.5	8.3	872	2	H95160	alan1-tRNA synthet
44	83	8.2	3430	1	GNMVKV	genome polyprotein
45	81.5	8.1	886	2	A37558	beta-amyloid-like

ALIGNMENTS

RESULT 1
149056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: 149056; S52866
R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J.Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: 149055; MUID:95052604; PMID:7963517
A:Accession: 149056
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648
R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu
A:Reference number: S52866
A:Accession: S52866
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-233 <KAM>
A:Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.5%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 2, 2e-22;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

Oy 11 PALVADFWGYKLRQKY-----V 28
Db 6 RELVVDPLSYKLSQSGYSSQPSDVEENRTAPDEETAEARETPSAINGNPMSHLADSPAV 65
Oy 29 CGAGCGEGPAD-----PLHQMRAAGDEEFTFRFRFFSDLAQLHTVPGSAOQFT 80
Db 66 NGA-TGSHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSLHITPGTAYOSFE 124
Oy 81 QVSDLLPQCGPWWGRLVAFVFGAALCAESVNMEMETLVQGVQVDMWVAYLETRLADWTHS 140
Db 125 QVNNELFRPDGVNWGRIVAFSFGALCVESVDKEMOVLVSRISWMTYLLNDHLEPWIOE 184
Oy 141 SGNMFEFTALYDGALEEARLRE--GNMAVTVTLTGAALGAL 183
Db 185 NCGMDTFVDLYGNMAAABESRKQGERFNRKFLTGMTVAGVVLGSL 229

RESULT 2
B47537
apoptosis regulator bcl-xl - human
N:Alternate names: bcl-2-related protein
;Contains: apoptosis regulator bcl-xs

C.Species: Homo sapiens (man)
C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
C.Accession: B47537; C47537
R.Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A.Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A.Reference number: A47537; MUID:93364977; PMID:8358789
A.Accession: B47537
A.Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-233 <BO1>
A.Cross-references: GB:L20121; NID:9510900; PIDN:CAA80661.1; PID:9510901
A.Accession: C47537
A.Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-69, G', 71-125, 189-233 <BO2>
A.Cross-references: GB:L20122; NID:9623236; PIDN:CAA80662.1; PID:9623237
C.Genetics:
A:Gene: GDB:BCL2L
A:Cross-references: GDB:228079
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis
F.1-233/Product: apoptosis regulator bcl-xl #status predicted <MAT>
F.1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 42.4%; Score 427.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 2.8e-32;
Matches 91; Conservative 23; Mismatches 53; Indels 51; Gaps 4;

QY 11 PALVADPFGYKLRQKQY-----VCGAGP---GEGPAA 39
DB 6 RELVVDPLSTYKLSQKGYMSQSFVDVENRTEAPECTSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQMRAGDEFEFRFRFTFSDLAQLHVTGPSAQQRTO 81
DB 66 NGATAHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFSLTNSQLHTPTGTAYQSFQ 125
QY 82 VSDLEFQGGPNMGRIVAFVFGALCAESVNMKEPPLVGQVDMVAVYLEFTLADWIMSS 141
DB 126 VNELFRDGVNMGRIIVAFVFGALCVESVDKEMQVLVSRIAMATYLNHLEPMIQEN 185
QY 142 GMAEFTALYGDALBEARLRLE--GNMASVTVLTGAVAGAL 183
DB 186 GMDTFVLDYGNMAAESRKQGRFNRWFLTGMTVAGVLLGSL 229

RESULT 3
S51761
BCL-X protein - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 28-Jul-2003
C.Accession: S51761; S51762
R.Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A.Reference number: S51761
A.Accession: S51761
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-233 <MIC>
A.Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57886.1; PID:9607177
A.Experimental source: embryonic; brain
A:Accession: S51762
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-125,189-233 <MI2>
A.Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178
A.Experimental source: embryonic; brain
A>Note: smaller form due to splicing
C.Genetics:
A:Introns: 125/3
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.1%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 5.3e-32;
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 13 LVADPFGYKLRQKQY-----VCG 30
DB 8 LVVFLSTYKLSQKGYMSQSFVDVENRTEAPECTSEMETPSAINGNPSWHLADSPAVNG 67
QY 31 AGPEGPAAD-----PLHQMRAGDEFEFRFRFTFSDLAQLHVTGPSAQQRTOV 82
DB 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFSLTNSQLHTPTGTAYQSFQV 126
QY 83 SDELFGGPNMGRIVAFVFGALCAESVNMKEPPLVGQVDMVAVYLEFTLADWIMSSG 142
DB 127 VNELFRDGVNMGRIIVAFVFGALCVESVDKEMQVLVSRIAMATYLNHLEPMIQEN 186
QY 143 GMAEFTALYGDALBEARLRLE--GNMASVTVLTGAVAGAL 183
DB 187 GMDTFVLDYGNMAAESRKQGRFNRWFLTGMTVAGVLLGSL 229

RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C.Species: Gallus gallus (chicken)
C.Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
A:Accession: A37332; S35453
R.Eguchi, Y.; Ewert, D.L.; Tanjimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A.Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: A37332
A.Status: nucleic acid sequence not shown
A.Molecule type: DNA
A.Residues: 1-233 <EGU>
A:Cross-references: EMBL:D11381
C.Genetics:
A:Introns: 189/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.0%; Score 423.5; DB 2; Length 233;
Best Local Similarity 38.0%; Pred. No. 6.5e-32;
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

QY 9 DTRALVADPFGYKLRQKGYCGAG-----PGGPAADP----- 41
DB 10 DNREIVLKRTHYKLSQKGYDMAAGDEPRPVPAPAPAAVAAGASSHHRRPPGSA 69
QY 42 -----LHQMRAGDEFEFRFRFTFSDLAQLHVTGPSAQQRTOVSD 84
DB 70 AASEVPAEGLRPAAPGVHLLRQAGDEFSSRRYQDFQMSGQLHTFTAHGRFVAIVE 129
QY 85 ELFGGPNMGRIVAFVFGALCAESVNMKEPPLVGQVDMVAVYLEFTLADWIMSSG 144
DB 130 ELFRDGVNMGRIIVAFVFGALCVESVNRKEMSLVDNLTATWTEYLNHLEPMIQEN 189
QY 145 AEFTALYGDALBEARLRLEGNMASVTVLTGAVAGALVTVGAFFASK 193
DB 190 DAFVELYGN---SMRPLDFSWISLKITLS-LVVGACITLGAYLGRK 233

RESULT 5
S24390
transforming protein (Bcl-2) homolog - chicken
C.Species: Gallus gallus (chicken)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 28-Jul-2003
C:Accession: S24390
R.Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A>Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A.Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-232 <CAZ>
A:Cross-references: EMBL:Z11961; NID:962969; PIDN:CAA78018.1; PID:562970
C:Superfamily: bcl apoptosis regulator, inhibitor type
C:Keywords: mitochondrion; transmembrane protein

Query Match 41.0%; Score 414; DB 2; Length 232;
Best Local Similarity 37.7%; Pred. No. 4.9e-31;
Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

Oy 9 DTRALVADPFVCYKLRQKGYVCAG-----PGEPAADP----- 41
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 10 DNREIVLKTIHYKLQSQRDYMAAGEDRPVPDPAPAAPAAVAAGAASHHRRSPARL 69
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 42 -----LHOAMRAAGDEFEFRFRFTFSDLAQLHTVPGSAQORFTVDS 85
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 70 LTVACPRRLGCAAPGVYHALRQGDEFSSRRYQGDFAQMSGQLHTFPPTATGRVAAYEE 129
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 86 LFQGGPWNGRLVAFVFVGALCAESVNKENEPYLGOVDMMVAVLETRLADMHSQSGWA 145
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 130 LFRDGVWVMVRIVAFEFEEFGVWCVESVKNREMSPLVDNIATWTETLNHLHNWIODNGMD 189
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 146 EFTLYDGDALEEARRLREGNWSAVRTVLTCGAVNLGLVTYGAFPAFK 193
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 AFVELYGN---SMRPLDFFSWISKLTLLS-LVLVGACTILGAYLGKH 232
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
TVHMU1
transforming protein bcl-2, splice form alpha - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change 28-Jul-2003
C:Accession: C37332; A29409; S02452; A24428; A27622; B27622
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4197, 1992
A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: C37332
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-239 <EGU>
A>Note: This report is a correction
R:Tsuji moto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A>Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for Burkitt's lymphoma
A:Reference number: A29409; MUID:86259760; PMID:3523487
A:Accession: A29409
A:Molecule type: mRNA
A:Residues: 1-95, 'A', '97-109, 'G', '111-236, 'S', '238-239 <TSU>
A:CROSS-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A>Note: this sequence has been corrected in reference A37332
R:Shero, M.; Jaeger, U.; Hockett, R.D.; Gruninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
EMBO J. 7, 123-131, 1988
A>Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene in human follicular lymphoma
A:Reference number: S02452; MUID:88196071; PMID:2834197
A:Accession: S02452
A:Molecule type: mRNA
A:Residues: 1-239 <SER>
R:Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A>Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer element
A:Reference number: A24428; MUID:87002488; PMID:2875799
A:Accession: A24428
A:Molecule type: mRNA
A:Residues: 1-58, 'T', '60-116, 'R', '118-239 <CLE>
A:CROSS-references: GB:M44745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R:Huh, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.C.; Bakshi, A.
Oncogene Res. 2, 263-275, 1988
A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A:Reference number: A27622; MUID:88217344; PMID:3285301
A:Accession: A27622
A:Molecule type: mRNA
A:Residues: 1-58, 'T', '60-239 <HUA>

A:Accession: B27622
A:Molecule type: DNA
A:Residues: 1-6,'S','B'-58,'T',60-128,'C',130-239 <HUA>
A>Note: The sequence was determined from the germline gene
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C:Genetics:
A:Gene: GDB:BCL2
A:Cross-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:description: blocks apoptosis in hematopoietic cells
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 40.8%; Score 411.5; DB 1; Length 236;
Best Local Similarity 37.0%; Pred. No. 8.8e-31;
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY DTRALVADVGKRLRKGVCGAG-----PGE----- 35
| | : : ||||| || ||
10 DNREIWMKIHYKLRSRGYEMDGDVGADPGAAPGAPGIRSSQPGRHPHPAASDPVART 69
36 -----GPADP----LHOAMRAAGDEFETRFRRTFSDLAAQLHTVTPGSACOR 78
70 SELPQTPAAGAAGAPLSPVPVPHLLTLRQAGDDFSRRYRRDRFAMWSQHLTLFTTAGR 129
QY FTQVSDELFGGGBNMGRIVAFVFGAALCAESYNKENEPVLGVQODMMVAYLETRLADI 138
130 FATVVEELPRDGVNMGRIVAFEFEGVMCVESVNREMPVLVDNIALMTTEYLNHHLHTWI 189
QY HSSGGAETALYGDALEEARLRREGNMASVTVLTGAVALGLLVTVGAFFASK 193
190 QDNQGWDAFEVELYG---PSMRPLPDFSWLSLTLSLAL-VGACITLGAYLGHK 239

Db 190 QDNQGWDAFEVELYG---PSMRPLPDFSWLSLTLSLAL-VGACITLGAYLGHK 239

RESULT 7
167432
BCL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_rev150n 26-Jul-1996 #text_change 28-Jul-2003
C:Accession: I67432
R.Tilly, J.L., Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.
A:Reference number: 153295; WUID:95129487; PMID:7828536
A:Accession: I67432
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: EMBL:U34964; NID:G1004378; PIDN:AAA77687.1; PID:G1004379
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;
Best Local Similarity 36.2%; Pred. No. 9.6e-31;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY DTRALVADVGKRLRKGV----- 27
| | : : ||||| || ||
10 DNREIWMKIHYKLRSRGYEMDGDSDASPLRARPTGIPSFOPESNRTPAVNHRTAART 69
QY 28 -----VCGAGPEGPADPDLHOAMRAAGDEFETRFRRTFSDLAAQLHTVTPGSACORFTQ 81
Db 70 SPLRPILVANAGPALSPVPVPHLLTLRQAGDDFSRRYRRDRFAMWSQHLTLFTTAGRPAT 129
QY 82 VSGELFGGGBNMGRIVAFVFGAALCAESYNKENEPVLGVQODMMVAYLETRLADIWISS 141
Db 130 VVEELPRDGVNMGRIVAFEFEGVMCVESVNREMPVLVDNIALMTTEYLNHHLHTWIODN 189
QY 142 GGAAEFTALYGDALAEARLRREGNMASVTVLTGAVALGLLVTVGAFFASK 193
Db 190 GGMDAWELEYG---PSMRPLPDFSWLSLTLSLAL-VGACITLGAYLGHK 236

RESULT 8
 153744 gene bcl-2 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 28-Jul-2003
 C:Accession: 153744
 R:Saco, T.; Irie, S.; Krajewski, S.; Reed, J.C.
 Gene 140, 291-292, 1994
 A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
 A:Reference number: 153744; PMID:94193015; PMID:8144041
 A:Accession: 153744
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236 <RES>
 A:Cross-references: GB:LI4680; NID:9408946; PIDN:AAA53662.1; PID:9408947
 C:Genetics:
 A:Gene: bcl-2
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.1%; Score 406; DB 2; Length 236;
 Best Local Similarity 35.8%; Pred. No. 2.8e-30;
 Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;

QY 9 DTRALVAFVGYKLRQKGY-----PG----- 27
 DB 10 DNRRLVKKYIKYKLSQGYEMTDGDESDAPLAAPTGIFSFQPSNRPVHRTAART 69
 QY 28 -----VCGAGPGEGRPADPLHQAARAGDEFETFRRTSDLAQLHVTGSAQQRFTQ 81
 DB 70 SPLRLPVNAGPALSPVPVHLLTRAGDDPSRRYRDFAMSSQLHLPTFARGRPAT 129
 QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLDWIHS 141
 DB 130 VVEELFRGVNMGRIVAFEFEGVWCVSVRKMSPLVDNIALMWTETLNRLHTWIDN 189
 QY 142 GMAEFPLALYGDGALAEARLRREGNMAVSRTVLTGAVALGALVTGVAFFASK 193
 DB 190 GMDAFVELYG---PSMRPLDFPSMLSKTLISLAL-VGACITLIGAYLGHK 236

RESULT 9
 TVMSA1 transforming protein bcl-2-alpha - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
 C:Accession: A25960; E37332
 R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
 Cell 49, 455-463, 1987
 A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
 A:Reference number: A90893; PMID:87187643; PMID:3032455
 A:Accession: A25960
 A:Molecule type: DNA
 A:Residues: 1-236 <NEG>
 A:Cross-references: GB:LI1532; GB:M16506; NID:9468336; PIDN:AAA37282.1; PID:9387109
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
 A:Reference number: A37332; PMID:92375724; PMID:1508712
 A:Accession: E37332
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: DNA
 A:Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>
 C:Genetics:
 A:Gene: BCL2
 A:Introns: 192/3
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 40.1%; Score 405; DB 1; Length 236;
 Best Local Similarity 37.1%; Pred. No. 3.5e-30;
 Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;

QY 9 DTRALVAFVGYKLRQKGYCGAG-----PG----- 34
 DB 10 DNRRLVKKYIKYKLSQGYEMTDGADADAAPLGAAPTGIFSFQPSNMPVHREMAART 69
 QY 35 -----EGRPADP---LHQAARAGDEFETFRRTSDLAQLHVTGSAQQRFTQ 81
 DB 70 SPLRLPVNAGPALSPVPVHLLTRAGDDPSRRYRDFAMSSQLHLPTFARGRPAT 129
 QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLDWIHS 141
 DB 130 VVEELFRGVNMGRIVAFEFEGVWCVSVRKMSPLVDNIALMWTETLNRLHTWIDN 189
 QY 142 GMAEFPLALYGDGALAEARLRREGNMAVSRTVLTGAVALGALVTGVAFFASK 193
 DB 190 GMDAFVELYG---PSMRPLDFPSMLSKTLISL-LPVGACITLIGAYLGHK 236

RESULT 10
 167431 BCL-X-Long - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Jul-2003
 C:Accession: 167431
 R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
 constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.
 A:Reference number: 153295; PMID:95129487; PMID:7828536
 A:Accession: 167431
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: EMBL:U34963; NID:91004376; PIDN:AAA7686.1; PID:91004377
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.1%; Score 404.5; DB 2; Length 233;
 Best Local Similarity 39.6%; Pred. No. 3.8e-30;
 Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;

QY 11 PALVADPFVGYKLRQKGY-----V 28
 DB 6 RELVDFLSTYKLSQGYSWQSFSDVENRTAPEETPERETPSAINGNPSMHLADSPAV 65
 QY 29 CGAGPGEGRPADP-----PLHQAARAGDEFETFRRTSDLAQLHVTGSAQQRFT 80
 DB 66 NGA-TGHSSSIDAREVLPMALVKQALRAAGDEFELRYRARASDLSQHLTPGVYQSF 124
 QY 81 QVSDLEFGGPNMGRVAFVFGAALCAESVKNEMEPVGVQVDMVAVLETRLDWIHS 140
 DB 125 QVNVNLFPGDVNMGRIVAFEFEGVWCVSVRKMSPLVDNIALMWTETLNRLHTWIDN 184
 QY 141 SGMAEFPLALYGDGALAEARLRREGNMAVSRTVLTGAVALGAL 183
 DB 185 NGMDTFVLDYGNMTAPESRKGQERFRNPLTGMTVAGVLLGSL 229

RESULT 11
 UC7383 B-cell lymphoma 2 protein - Chinese hamster
 C:Species: Citellus griseus (Chinese hamster)
 C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 28-Jul-2003
 C:Accession: UC7383
 R:Tomicic, M.T.; Christmann, M.; Kaina, B.
 Biochem. Biophys. Res. Commun. 275, 899-903, 2000
 A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
 A:Reference number: UC7383
 A:Contents: Ovary
 A:Accession: UC7383
 A:Molecule type: mRNA
 A:Residues: 1-236 <TOM>
 A:Cross-references: GB:Au271720
 C:Comment: This protein has anti-apoptotic function, and supports cell survival.
 C:Genetics:

transforming protein (bcl-2-beta) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003

C:Accession: B37332; S35452

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: B37332

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-216 <EGU>

A:Cross-references: EMBL:D11381; EMBL:D11382

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 35.3%; Score 356; DB 2; Length 216;

Best Local Similarity 38.4%; Pred.No. 1.1e-25;

Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps 2;

```

QY      9 DTRALVADPVGKLRKRGVVGAG-----PGEGRPADP----- 41
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     10 DNRRLVLTQIYKLSQKRGIDWAGSDRPVPAPAPAAAPAAVAAAGASSHHRPBPQSA 69
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     42 -----LHQAARAGDEPETERFRRTFSDLAQLHVTGSAQQRFTQVSD 84
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     70 AASEVPAPAGLRPAPPGVHLALRQAGDEFRRYQRDFQMSQGLHPTFAHGRFVAIVE 129
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     85 ELFGGPNWGRVAFVFGAALCAESVNEKMEPLVGQVQVDMVAVILETRLADWHSQGM 144
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     130 ELFRDGVNMGRIVAFEFEGVNCVSVNREMSPLVDNIATWMTXYLNRIHNMIDNGM 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     145 AEFTA 149
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     190 VRACA 194

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Search completed: February 26, 2004, 11:15:02
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:07:17 ; Search time 18 Seconds

(without alignments)
558.308 Million cell updates/sec

Title: US-09-508-745-4

Perfect score: 1009

Sequence: 1 MATPASTPDRALVADRVG.....LTGAVLALGALVTGAFPAASK 193

Scoring table: BLOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1009	100.0	193	1	BCLM_MOUSE
2	1000	99.1	193	1	BCLW_HUMAN
3	650.5	64.5	228	1	ARI_XENLA
4	432.5	42.5	229	1	BCLX_CHICK
5	431.5	42.8	233	1	BCLX_PIG
6	428.5	42.5	233	1	BCLX_MOUSE
7	428.5	42.5	233	1	BCLX_RAT
8	427.5	42.4	233	1	BCLX_HUMAN
9	423.5	42.0	233	1	BCLX_CHICK
10	415.5	41.2	229	1	BCL2_BOVIN
11	413	40.9	236	1	BCL2_RAT
12	412	40.8	236	1	BCL2_MOUSE
13	411.5	40.8	239	1	BCL2_HUMAN
14	402	39.8	236	1	BCL2_CRICO
15	369	36.6	204	1	ARI1_XENLA
16	175.5	17.4	208	1	BAK_MOUSE
17	171	16.9	211	1	BAK_HUMAN
18	168	16.7	211	1	BAK2_HUMAN
19	156.5	15.5	192	1	BAKX_MOUSE
20	155.5	15.4	192	1	BAKX_RAT
21	154	15.3	192	1	BAKX_HUMAN
22	151	15.0	280	1	CRD9_HUMAN
23	148	14.7	192	1	BAKX_BOVIN
24	147.5	14.6	218	1	BAKX_HUMAN
25	142	14.1	177	1	NR13_CRIC
26	138.5	13.7	143	1	BAKX_HUMAN
27	137.5	13.6	271	1	CEPD9_CABER
28	116	11.5	175	1	BFL1_HUMAN
29	116	11.5	175	1	BFL1_HUMAN
30	115	11.4	194	1	BCLB_HUMAN
31	105	10.4	172	1	BFL1_MOUSE
32	99.5	9.9	179	1	BAR_ASFM2
33	98.5	9.8	179	1	BAR_ASFB7

ALIGNMENTS

RESULT 1	ID	BCLM_MOUSE	STANDARD	PRT	193 AA
AC	P70345				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).				
GN	BCL2L2 OR BCLM.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=C57BL/10J;				
RC	MEDLINE=96358615; PubMed=9500547;				
RX	Ross A.J., Maymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,				
RA	Russell L.D., Macgregor G.R.,				
RT	"testicular degeneration in Bclw-deficient mice.";				
RL	Nat. Genet. 18:251-256(1998).				
CC	- FUNCTION: Promotes cell survival.				
CC	- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and				
CC	in a wide range of tissues, with highest levels in brain, colon,				
CC	and salivary gland.				
CC	- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic				
CC	function.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.				
CC	- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.				
CC	- SIMILARITY: Belongs to the Bcl-2 family.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: U59746; AAB09056.1; -				
DR	EMBL: AF030769; AAB86430.1; -				
DR	HSSP: Q07817; IMAZ.				
DR	MGD: MGI:108052; Bcl2l2.				
DR	InterPro: IPR000712; Bcl2_BH.				
DR	InterPro: IPR003093; Bcl2_BH4.				
DR	InterPro: IPR002475; Bcl2_family.				
DR	Pfam: PF00452; Bcl-2; 1.				

34	98.5	9.8	179	1	BAR_ASFB4	007818 african swi
35	87.5	8.7	660	1	SOHC_BRAJA	P54924 bradyrhizob
36	87	8.6	3433	1	POLG_KUNJM	P14335 k genome po
37	86	8.5	275	1	DAPB_AGR5	Q8uiv8 agrobacteri
38	85.5	8.5	358	1	GLNA_LACSA	P23712 lactuca bat
39	83.5	8.3	872	1	SYA_STRPN	Q97q48 streptococc
40	83.5	8.3	872	1	SYA_STRPN	Q8ddpc7 streptococc
41	83	8.2	3430	1	POLG_WNV	P06535 w genome po
42	81.5	8.1	887	1	A4_DROME	P14599 drosophila
43	80.5	8.0	236	1	YJ94_ARCFU	O28285 archaeglob
44	80.5	8.0	1440	1	POLG_JAEVN	P14403 j genome po
45	80.5	8.0	3432	1	POLG_JAEVU	P32886 j genome po

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DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS00063; BH4_2; 1.
DR Apoptosis.
KM DOMAIN 9 BH4.
FT DOMAIN 85 BH1.
FT DOMAIN 136 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 1009; DB 1; Length 193;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60
DB 1 MATPASTPTRALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTPTGSAQOQRTQVSDLEFQGGPMWGRVAFVFGAALCAESVKNKEPVLV 120
DB 61 FSDLAQLHVTPTGSAQOQRTQVSDLEFQGGPMWGRVAFVFGAALCAESVKNKEPVLV 120
QY 121 QYQDMMVAVLETRLDWIMHSSGGAFFTLVYDGALEEARLRREGVMSVRTLGAVAL 180
DB 121 QYQDMMVAVLETRLDWIMHSSGGAFFTLVYDGALEEARLRREGVMSVRTLGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 2
BCLW HUMAN STANDARD; PRT; 193 AA.
ID BCLW HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-1 (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLW OR KIA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RA "bcl-1", a novel member of the bcl-2 family, promotes cell survival.";
RT Oncogene 13:665-675(1996).
RN [2];
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIA0201-KIA0289) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RN [3];
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carinini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: U59747; AAB09055.1; -.
CC EMBL: D87461; BAA19666.1; -.
CC EMBL: BC021198; AAH21198.1; -.
CC HSP: O07817; IMAZ.
CC GeneW: HGNC:995; BCL2L2.
CC MIM: 601931; -.
CC GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO: GO:0006916; P:anti-apoptosis; TAS.
CC GO: GO:0007283; P:spermatogenesis; TAS.
CC InterPro: IPR000712; BCL2_BH.
CC InterPro: IPR003093; BCL2_BH4.
CC InterPro: IPR002475; BCL2_FAMILY.
CC Pfam: PF00452; BCL-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PS00062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS00063; BH4_2; 1.
CC Apoptosis.
KM DOMAIN 9 BH4.
FT DOMAIN 85 BH1.
FT DOMAIN 136 BH2.
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match
Best Local Similarity 99.1%; Score 1000; DB 1; Length 193;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60
DB 1 MATPASTPTRALVADPFGYKLRQGYCGAGPGGPAADPLHQMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTPTGSAQOQRTQVSDLEFQGGPMWGRVAFVFGAALCAESVKNKEPVLV 120
DB 61 FSDLAQLHVTPTGSAQOQRTQVSDLEFQGGPMWGRVAFVFGAALCAESVKNKEPVLV 120

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Db      61 FSDLAQLHTVPSGAQORFTQVSDLEFGCGPNMGRVAFVFGAALCAESVKNEMEPLVG 120
Qy      121 QVQWMMVAYLETRLADWTHSSGWAEPFALYGDGALBEARLRREGMNASVTVLTGVAL 180
Db      121 QVQWMMVAYLETRLADWTHSSGWAEPFALYGDGALBEARLRREGMNASVTVLTGVAL 180
Qy      181 GALVTGAFPAASK 193
Db      181 GALVTGAFPAASK 193

RESULT 3
ARI_XENLA
ID _ARI_XENLA STANDARD; PRT; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2 (Xenopus laevis).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-2.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X82462; CA57845.1; -.
DR HSSP; Q07817; IMA2.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KM Apoptosis; Transmembrane.
FT NON_TER 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;
Query Match 64.5%; Score 650.5; DB 1; Length 228;
Best Local Similarity 68.5%; Pred. No. 4e-51;
Matches 126; Conservative 20; Mismatches 35; Indels 3; Gaps 1;
Qy 10 TRALVADFGVYKLRQKGVGAGGEGRAADPLQAMAAADDEFTRRRFTSOLAQLH 69

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Db      48 SRALVEDLVRYKLCQORSLV---PEPSGASCALHSARAAAGDEFEERFRQAFSEISYQIH 104
Qy      70 VTPSSAQORFTQVSDLEFGCGPNMGRVAFVFGAALCAESVKNEMEPLVGQVQWMMVAY 129
Db      105 VTPGTAARPAEVAAGSLFFQGVMMGRVAFVFGAALCAESVKNEMSPLEPRIDMMVTVY 164
Qy      130 LETRLADWTHSSGWAEPFALYGDGALBEARLRREGMNASVTVLTGVALGALVTGAF 189
Db      165 LETRLADWTHSSGWAEPFALYGDGALBEARLRREGMNASVTVLTGVALGALVTGAL 224
Qy      190 FASK 193
Db      225 FASK 228

RESULT 4
BCLX_CHICK
ID _BCLX_CHICK STANDARD; PRT; 229 AA.
AC Q07815; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=910311;
RA Villagra X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -1- FUNCTION: Dominant regulator of apoptotic cell death. The long
CC isoform promotes apoptosis (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07816-2; Sequence=VSP_000514;
CC -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC development.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function. Intact BH1 and BH2 domains are required for anti-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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 CC EMBL; Z23110; CA80657.1; -
 CC EMBL; U26645; AAB0767.1; -
 CC PIR; A47537; A47537.
 DR HSPB; P53563; IAF3.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 82 96 BH3.
 FT DOMAIN 125 144 BH1.
 FT DOMAIN 176 191 BH2.
 FT TRANSMEM 206 223 POTENTIAL.
 FT VARSPPLIC 185 229 ERFVLYGNNAAELRKQGFENKWLGTGATVAGVLLLGST.
 FT LSRK -> VRTALP (in isoform Short).
 FT /FTID=VSP 000514.
 SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C059DA CRC64;

Query Match 42.8%; Score 432.5; DB 1; Length 229;
 Best Local Similarity 41.7%; Pred. No. 1.3e-31;
 Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADPFYGYLTKRKQGY-----VCGAPRGESR----- 37
 DB 6 RELVLDIFVSYKLSQKSGHCHSELEEDENRTDAEAKNDSDVANGSPSWHPAGHYVNGAT 65
 QY 38 -----AADPLHQAARAGDEFETFRPTFSDLAQLAHVTPGSAOQRTQVSD 85
 DB 66 VARSSELEHETIRADIVRAQALDADGEFLKRRRAFSDLTSGHITPGTAYGSEFGVYNE 125
 QY 86 LFQGGPNWGRVAVFVFGAALCAESVYKMEKPELVQGVQDMMVAVYLETRIADVIHSSGMA 145
 DB 126 LFHDGVNMGRIIVAFPSFGALCVESYDKEMRVLVGRIVSMWTYTLTDHIDPWIQENGWE 185
 QY 146 EFTALYGCALFEARLRREGNMAVTVLTGAVNAGALVTGAFPAFK 193
 DB 186 RVPDLYGNNA---AAELRKQGFENKWLGTGATVAGVLL-LGSLLSRK 229

RESULT 5
 BCL2_PIG STANDARD; PRT; 233 AA.
 ID BCL2_PIG
 AC 077737;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99171363; PubMed=10072723;
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Damer D.;
 RT "Quantification of cardioprotective gene expression in porcine
 RT short-term hibernating myocardium.";

RL J. Mol. Cell. Cardiol. 31:147-158 (1999).
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
 CC apoptotic activity is inhibited by association with SIVA isoform
 CC 1. Inhibits activation of caspases (By similarity). Appears to
 CC regulate cell death by blocking the voltage-dependent anion
 CC channel (VDAC) by binding to it and preventing the release of the
 CC caspase activator, cytochrome c, from the mitochondrial membrane.
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
 CC similarity). Heterodimerization with BAX does not seem to be
 CC required for anti-apoptotic activity (By similarity). Isoform Bcl-
 CC X(L) binds to SIVA isoform 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 CC envelope (By similarity).
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 CC with other Bcl2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
 CC apoptotic activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
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CC EMBL; AJ001203; CA04597.1; -
 DR HSPB; Q07817; IMAZ.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Apoptosis; Mitochondrion; Transmembrane.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226 POTENTIAL.
 SQ SEQUENCE 233 AA; 26061 MW; 1BBF6FA0441912B2 CRC64;

Query Match 42.8%; Score 431.5; DB 1; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.6e-31;
 Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;
 QY 11 RALVADPFYGYLTKRKQGY-----V 28
 DB 6 RELVLDIFVSYKLSQKSGHCHSELEEDENRTDAEAKNDSDVANGSPSWHPAGHYVNGAT 65
 QY 29 CGAGPGEPPAD-----PLHQMARAGDEFETFRPTFSDLAQLAHVTPGSAOQRT 80
 DB 66 NGA-TGHSSSLDAREVIMAAVKQALREAGDEFELRRARAFSDLTSGHITPGTAYGSE 124
 QY 81 QVSDLEFQGGPNWGRVAVFVFGAALCAESVYKMEKPELVQGVQDMMVAVYLETRIADVIH 140
 DB 125 QVLNLEFRDGVNMGRIIVAFPSFGALCVESYDKEMQVLSRIATWMAATYLNHLEPWIQ 184

Oy 141 SGCWAEFTALYDGLBEARLRE--GNWASVTRVLTGVALGAL 183
 Db 185 NGMDTFVELYGNNAABSRKGRFNRWPLTGMTAGVLLGSL 229
 RESULT 6
 BCLX_MOUSE STANDARD; PRT; 233 AA.
 AC 064373; 060657; 061338;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN BCL2L1 OR BCL2L2 OR BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2A4B;
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=9531139; PubMed=7607090;
 RA Gonzalez-Garcia M., Perez-Ballesteros R., Ding L., Duan L., Boise L.H.,
 RA Thompson C.B., Nunez G.;
 RT "bcl-2L is the major bcl-2 mRNA form expressed during murine
 RT development and its product localizes to mitochondria."
 RL Development 120:3033-3042(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).
 RC TISSUE=Pre-B cell;
 RX MEDLINE=95052604; PubMed=7663517;
 RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
 RT "Cloning and molecular characterization of mouse bcl-x in B and T
 RT lymphocytes."
 RL J. Immunol. 153:4388-4398(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=98051053; PubMed=9390687;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 RT apoptosis in T cells."
 RL Immunology 7:629-639(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97289584; PubMed=9144489;
 RA Grillo D.A., Gonzalez-Garcia M., Eklterae D., Duan L., Inohara N.,
 RA Ohta S., Seldin M.F., Nunez G.;
 RT "Genomic organization, promoter region analysis, and chromosome
 RT localization of the mouse bcl-x gene."
 RL J. Immunol. 158:4750-4757(1997).
 RN [6]
 RP FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
 RP apoptotic activity is inhibited by association with SIVA isoform
 RP 1. Inhibits activation of caspases (By similarity). Appears to
 RP regulate cell death by blocking the voltage-dependent anion
 RP channel (VDAC) by binding to it and preventing the release of the
 RP caspase activator, cytochrome c, from the mitochondrial membrane.
 RP The Bcl-X(S) isoform promotes apoptosis.
 RN [7]
 RP SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
 RP similarity). Heterodimerization with BAX does not seem to be
 RP required for anti-apoptotic activity (By similarity). Isoform Bcl-
 RP X(L) binds to SIVA isoform 1 (By similarity).
 RN [8]
 RP SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 RP envelope for Bcl-X(L). Cytoplasmic for Bcl-X(delta-TM).
 RN [9]
 RP ALTERNATIVE PRODUCTS:
 RP Event=Alternative splicing; Named isoforms=4;
 RN Name=BCL-X(L);

CC IsoId=Q64373-1; Sequence=Displayed;
 CC Name=BCL-X(S);
 CC IsoId=Q64373-2; Sequence=VSP_000517;
 CC Name=BCL-X(beta);
 CC IsoId=Q64373-3; Sequence=VSP_000518;
 CC Name=BCL-X(delta-TM);
 CC IsoId=Q64373-4; Sequence=VSP_000519;
 CC TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 CC brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-
 CC TM) expression is enhanced in B and T lymphocytes that have been
 CC activated.
 CC -1- DEVELOPMENTAL STAGE: Bcl-X(beta) is expressed in both embryonal
 CC and postnatal tissues, whereas Bcl-X(L) is predominantly found in
 CC postnatal tissues.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 CC with other Bcl2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
 CC apoptotic activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
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 CC -----
 CC EMBL; X83574; CAAS8557.1; -;
 CC EMBL; L35049; AAAS1039.1; -;
 CC EMBL; L35048; AAAS1040.1; -;
 CC EMBL; U10102; AAAB2174.1; -;
 CC EMBL; U10101; AAAB2173.1; -;
 CC EMBL; U10100; AAAB2172.1; -;
 CC EMBL; U51279; AAC53460.1; -;
 CC EMBL; U78031; AAB96881.1; -;
 CC EMBL; U78030; AAB96881.1; JOINED.
 CC PIR; I49055; I49055.
 CC PIR; I49056; I49056.
 CC PIR; I49057; I49057.
 CC HSSP; P53563; IAF3.
 CC MGD; MGI:88139; Bcl2L1.
 CC InterPro; IPR000712; Bcl2_BH.
 CC InterPro; IPR003093; Bcl2_BH4.
 CC InterPro; IPR004751; Bcl2_Family.
 CC InterPro; IPR004725; Bcl2_Reg.
 CC Pfam; PF00452; Bcl-2; 1.
 CC Pfam; PF02180; BH4; 1.
 CC SMART; SM00337; BCL; 1.
 CC SMART; SM00265; BH4; 1.
 CC TIGRFAMs; TIGR00865; bcl-2; 1.
 CC PROSITE; PS50062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4; 1.
 CC PROSITE; PS01261; BH4_1; 1.
 CC PROSITE; PS50063; BH4_2; 1.
 CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
 KW DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226 POTENTIAL.
 FT VARSPLIC 126 188 Missing (in isoform BCL-X(S)).
 FT VARSPLIC 189 233 /FTid=VSP_000517.
 FT DTFDLYGNNAABSRKGRFNRWPLTGMTAGVLLGSL
 FT FSRK -> VRTTPLVCPPLACVSLGCHP (in isoform

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FT FT BCL-X(beta)).
FT FT /FTID=VSP_000518.
FT FT LYNNAABSRKGRFRNRLTGMVAVGLLGLSFRSK
FT FT --> GHDCGCGSAGLTLOSEVVRH (in isoform
FT FT BCL-X(delta-TM)).
FT FT /FTID=VSP_000519.
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072B CRC64;
Query Match 42.5%; Score 428.5; DB 1; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.9e-31;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPFGYKLRQKQY-----V 28
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
Db 6 RELVVDPLSYKLSQGYGWSQPSDVENRTEAPETEARETRPSAINGNPSWHLDSPAV 65
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
QY 29 CGAGGEGEPAD-----PLHQAMRAAGDFEFRFRTEEDLAAQLHVTGSGQQRFT 80
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
Db 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRRAFSDLTSLHITPTAYQSFE 124
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
QY 81 QVSDSLFOGCGPWGRLVAFVFGALCAESVKNKEBPLVQGVQDMVAVLETRRLADWTHS 140
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
Db 125 QVNVNLFPRGVWGRIVAFSPFGALCVESVDKEQVLSRLASWMTATYLDNDLHPWIOE 184
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
QY 141 SGMAEFTALYGDALIEARRLR--GNWASYRTVLTGAVLALGAL 183
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
Db 165 NGGMPTFVDLYGNMAAESRKQGERFNRFLTGMVAVAGVVLGSL 229
| | | | | | | | | | | | | | | | | | | | |
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RA Arizumi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA Morikawa K.;
RT "Crystal structure of rat Bcl-XL. Implications for the function of
RT the Bcl-2 protein family."
RL J. Biol. Chem. 272:27866-27892(1997).
CC -I- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (By similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.
CC -I- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC X(L) binds to SIVA isoform 1 (By similarity).
CC -I- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Bcl-X(L);
CC IsoId=P53563-1; Sequence=Displayed;
CC Name=Bcl-X(S); Sequence=VSP_000520;
CC IsoId=P53563-2;
CC Name=Bcl-X(beta);
CC IsoId=P53563-3; Sequence=VSP_000521;
CC -I- TISSUE SPECIFICITY: Expressed in cerebellum, heart, and thymus. In the
CC specifically expressed in cerebellum, heart, and thymus. In the
CC ovary, the predominant form is Bcl-X(L), with a small but
CC detectable level of Bcl-X(S).
CC -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -I- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity (By similarity).
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -I- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X82537; CAAS7886.1; -
DR EMBL, X82537; CAAS7887.1; -
DR EMBL, U10579; AAB19287.1; -
DR EMBL, U72350; AAB17353.1; -
DR EMBL, U72349; AAB17352.1; -
DR EMBL, U34963; AAB7686.1; -
DR EMBL, S76513; AAC60701.2; ALT_INIT.
DR EMBL, S78284; AAC60702.1; -
DR PIR, 167431; 167431.
DR PIR, S51761; S51761.
DR PDB, 1AF3; 07-JUL-97.
DR InterPro, IPR000712; Bcl2_BH.
DR InterPro, IPR003093; Bcl2_BH.
DR InterPro, IPR002475; Bcl2_family.
DR InterPro, IPR004725; Bcl2_reg.
DR Pfam, PF00452; Bcl-2; 1.
DR Pfam, PF02180; BH4; 1.
DR SMART, SM00337; BCL; 1.
DR SMART, SM00265; BH4; 1.
DR TIGRFAMs, TIGR00865; bcl-2; 1.
DR PROSITE, PS50062; BCL2_FAMILY; 1.
DR PROSITE, PS01080; BH1; 1.
DR PROSITE, PS01258; BH2; 1.

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DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4.1; 1.
 DR PROSITE; PS50063; BH4.2; 1.
 KM Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
 KM 3D-structure.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226 POTENTIAL.
 FT VAAPPLIC 126 188 Missing (in isoform Bcl-X(S)).
 FT VAAPPLIC 189 233 /FtId=VSP_000520.
 FT VAAPPLIC 189 233 DTPVDLYGNNAASRKGQERFNRMFLTGMTAGVLLGSL
 FT PSRK -> VRTTPLYCPLVCLSSVYEINCFMSPGMVED
 FT IDYSGDIPGL (in isoform Bcl-X(beta)).
 FT /FtId=VSP_000521.
 FT R -> Q (IN REF. 1).
 FT F -> S (IN REF. 2).
 FT A -> E (IN REF. 2).
 FT I -> L (IN REF. 4).
 FT A -> V (IN REF. 4).
 FT FF -> SS (IN REF. 4).
 FT A -> T (IN REF. 4).
 FT A -> P (IN REF. 4).
 FT HELIX 4 19
 FT TURN 20 21
 FT TURN 25 28
 FT TURN 82 83
 FT HELIX 84 100
 FT HELIX 106 112
 FT TURN 116 127
 FT HELIX 120 127
 FT HELIX 128 131
 FT TURN 132 133
 FT HELIX 137 156
 FT TURN 157 158
 FT TURN 160 161
 FT HELIX 162 177
 FT TURN 178 184
 FT HELIX 179 184
 FT TURN 185 186
 FT HELIX 187 195
 FT SEQUENCE 233 AA; 26158 MW; 2B62B6C63864BC8F CRC64;
 Query Match 42.5%; Score 428.5; DB 1; Length 233;
 Best Local Similarity 41.3%; Pred. No. 2.9e-31;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
 QY 11 RAIVADPVGVYKLRKQGY-----V 28
 DB 6 RELVVDPLSTYKLSQKGYSWQSFDVENRTAPEBTEBERETPSALINGNPSMHLADSPAV 65
 QY 29 CGAGPGCGPAD-----PLHQAMRAAGDEFETFRPTSDLAQLHTVPGSAQGRFT 80
 DB 66 NGA-TGHSSTSLDAEVIEMAVKQALRAAGDEFELRYRAASDLSQHLTPGTAQSF 124
 QY 81 QVSDLEFGQGFNWRGLVAFVFGAALCAESVKNKEMEPLVGVQVDMVAVLETRLDWTHS 140
 DB 125 QVNVIELFRDGVNWRIVAFSFGALCVESVDKEMQVLSRIASMMATYLDHLEPWIOE 184
 QY 141 SGGNAEFALYGDGALAEARLR--GNWASVRYLVGAVALLGL 183
 DB 185 NGWMDTFVDLYGNNAASRKGQERFNRMFLTGMTAGVLLGSL 229

GN BCL2L1 OR BCL2L OR BCLX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
 RX MEDLINE=93364977; PubMed=8358789;
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 Tuika L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 of apoptotic cell death."
 RL Cell 74:597-608(1993).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
 RA Inohara N., Ohta S.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM X(L)).
 RC TISSUE=lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein W.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP MUTAGENESIS OF GLY-138 AND HETERO-DIMERIZATION.
 RX MEDLINE=95372373; PubMed=7644501;
 RA Sedlak T.W., Oltsai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
 Korsmeyer S.J.;
 RT "Multiple Bcl-2 family members demonstrate selective dimerizations
 with Bax."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
 [5]
 RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
 RX MEDLINE=96170038; PubMed=859636;
 RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
 Korsmeyer S.J.;
 RT "Bax-independent inhibition of apoptosis by Bcl-XL."
 RL Nature 379:554-556(1996).
 [6]
 RP INTERACTION WITH SIVA.
 RX MEDLINE=22008092; PubMed=12011449;
 RA Wu L., Chu F., Cheng Y., Sun X., Borthakur A., Ramarao M., Pandey P.,
 Wu M., Schlossman S.F., Prasad K.V.S.;
 RT "Siva-1 binds to and inhibits Bcl-X(L)-mediated protection against UV
 radiation-induced apoptosis."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).
 [7]
 RP STRUCTURE BY NMR OF 1-209.
 RX MEDLINE=97172562; PubMed=9020082;
 RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
 Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mann A.J.,
 Thompson C.B., Fesik S.W.;
 RT "Structure of Bcl-XL-Bak peptide complex: recognition between
 regulators of apoptosis."
 RL Science 275:983-986(1997).

[8]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
 RP MEDLINE=96256675; PubMed=8692274;
 RX Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
 RA Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
 RA Ng S.L., Pesik S.W.;
 RT "X-Ray and NMR structure of human Bcl-XL, an inhibitor of programmed
 cell death.";
 RL Nature 381:335-341 (1996).
 (9)
 RN CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
 RP MEDLINE=98118550; PubMed=9435230;
 RX Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
 RA Takahashi A., Kaestan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,
 RA Hardwick J.M.;
 RT "Modulation of cell death by Bcl-XL through caspase interaction.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559 (1998).
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
 apoptotic activity is inhibited by association with SIVA isoform
 1. Inhibits activation of caspases (by similarity). Appears to
 regulate cell death by blocking the voltage-dependent anion
 channel (VDAC) by binding to it and preventing the release of the
 caspase activator, cytochrome c, from the mitochondrial membrane.
 CC The Bcl-X(S) isoform promotes apoptosis.
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.
 CC Heterodimerization with BAX does not seem to be required for anti-
 apoptotic activity. Isoform Bcl-X(L) binds to SIVA isoform 1.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 envelope (by similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Bcl-X(L);
 CC IsoId=Q07817-1; Sequence=Displayed;
 CC Name=Bcl-X(S);
 CC IsoId=Q07817-2; Sequence=VSP_000515;
 CC Name=Bcl-X(beta);
 CC IsoId=Q07817-3; Sequence=VSP_000516;
 CC -1- TISSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells
 that undergo a high rate of turnover, such as developing
 lymphocytes. In contrast, Bcl-X(L) is found in tissues containing
 long-lived postmitotic cells, such as adult brain.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 with other Bcl2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 cleaved protein, lacking the BH4 domain, has pro-apoptotic
 activity.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, Z23116; CAAB0662.1; -
 DR EMBL, Z23115; CAAB0661.1; -
 DR EMBL, U72398; AAB17354.1; -
 DR EMBL, BC019307; AAH19307.1; -
 DR PIR, B47537; B47537.
 DR PIR, J80203; J80203.
 DR PDB, 1BXL; 29-OCT-97.
 DR PDB, 1LXL; 21-APR-97.
 DR PDB, 1MAZ; 21-APR-97.
 DR PDB, 1G5J; 07-FEB-01.
 DR PDB, 1G5M; 21-MAR-01.
 DR PDB, 1G5H; 13-JUN-01.

DR Genew; HGNC:992; BCL2L1.
 DR MIM: 600039; -
 DR GO: GO:0005739; C:mitochondrion; TAS.
 DR GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO: GO:0006916; F:anti-apoptosis; TAS.
 DR GO: GO:0008637; P:apoptotic mitochondrial changes; TAS.
 DR GO: GO:0008634; P:negative regulation of survival gene products; TAS.
 DR InterPro: IPR00712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRfam: TIGR00865; bcl-2; 1.
 DR PROSITE: PS00062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS00663; BH4_2; 1.
 DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
 KW 3D-structure.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226 POTENTIAL.
 FT SITE 61 62 CLEAVAGE (BY CASPASE-1).
 FT VARSPPLIC 126 188 Missing (in isoform Bcl-X(S)).
 FT VARSPPLIC 189 233 /FtId=VSP_000515.
 FT VARSPPLIC 189 233 DIFVELYGNMAAESRKGGRFNNRFLTGMTVAGVLLGSL
 FT VARSPPLIC 189 233 FSRK -- YRKRPVCPSPSLASGSPFALLLYFLGLMVI
 FT VARSPPLIC 189 233 VGDVDS (in isoform Bcl-X(beta)).
 FT FTId=VSP_000516.
 FT MUTAGEN 61 61 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
 FT MUTAGEN 131 133 FRD->VRA: NO HETERODIMERIZATION WITH BAX.
 FT MUTAGEN 135 137 VNM->ALL: LOSS OF ANTI-APOPTOTIC
 FT MUTAGEN 138 140 ACTIVITY.
 FT MUTAGEN 138 140 GRI->ELN: LOSS OF ANTI-APOPTOTIC
 FT MUTAGEN 138 138 ACTIVITY.
 FT MUTAGEN 138 138 G->A: NO HETERODIMERIZATION WITH BAX.
 FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.
 FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
 FT MUTAGEN 176 176 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
 FT MUTAGEN 188 189 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
 Query Match 42.4%; Score 427.5; DB 1; Length 233;
 Best Local Similarity 41.3%; Pred. No. 3.6e-31;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
 QY 11 PALVADPVGVKLRQKQY-----Y 28
 DB 6 RELVVDPLSTYKLSQSGVMSQSDVEENRTEAPEGTESEMETPSALNGNPSWHLADSPAY 65
 QY 29 CGAGGGEGBPAD-----PLHQMRAGAAGEFERFRFRRTSDLAQCHVTPGSGQQQRT 80
 DB 66 NGA-TGSHSSSTDAREVIMPAVKQALREAGGEFFELRYRRASDLSQDLHTPGTVQSF 124
 QY 81 QVSDLEFGGPRVWGVAFVFGAALCAESYVKEKEPVGQVDMVAVYLETRLADWTHS 140
 DB 125 QVNELEFRDGVNMGVIVAFSFGALCVESVDKEQVLSKRAMMATYLLNDHLEPWIQE 184
 QY 141 SGGMAEFTALYGDGALFEARRLRE--GNMVASRTVLTGAVALGAL 183
 DB 185 NCGMDTFVEIYGNMAAESRKGGRFNNRFLTGMTVAGVLLGSL 229
 RESULT 9
 BCL2_CHICK
 ID_BCL2_CHICK STANDARD; PRT; 233 AA.

AC 000709:
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92375724; PubMed=1508712;
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 in a variety of tissues including lymphoid and neuronal organs in
 adult and embryo."
 RT Nucleic Acids Res. 20:4187-4192 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Caralz-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 homologue of the Bcl-2 oncoprotein."
 RL Blochim. Biophys. Acta 1132:109-113 (1992).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2
 domains, and is necessary for anti-apoptotic activity (by
 similarity). Also interacts with APAF-1 and Raf-1 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 kidney, heart, ovary and brain, with the highest levels in the
 thymus. In the embryo, highly levels expressed in all tissues with
 high levels in the bursa of Fabricius.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 for interaction with Raf-1 (by similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
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 or send an email to license@ebi.ac.uk).

DR SMART: SMO0265; BH4_1.
 DR TIGRFAMs: TIGR00865; bcl-2_2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1_1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 DR Apoptosis; Transmembrane; Mitochondrion.
 KW Apoptosis; Transmembrane; Mitochondrion.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 87 101 BH3.
 FT DOMAIN 130 149 BH1.
 FT DOMAIN 181 196 BH2.
 FT TRANSMEM 208 228 POTENTIAL.
 FT TRANSMEM 64 64 E -> S (IN REF. 2).
 FT CONFLICT 67 82 GSAASEVPPAEGRP -> ARLLVRCPLRGCA
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 SQ SEQUENCE 233 AA; 25687 MM; 525255ACB6E4C3D CRC64;
 Query Match 42.0%; Score 423.5; DB 1; Length 233;
 Best Local Similarity 38.0%; Pred. No. 8.2e-31;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;
 QY 9 DTRALVADFPYGYKLRQGYVCGAG-----PGSGPAAADP----- 41
 DB 10 DNRSLVLYHYKLSQGYMAAGEDRPVPAPAPAAVAAGASHHREPPGSA 69
 QY 42 -----LHQMRAAGDEFETFRFTSDLAQAHVTPGSAQOGRFTQVD 84
 DB 70 AASVPPAEGRLPAPPGVHLALRQAGDEFRRYDRDRQSGQLHPTFHAGFVAIVE 129
 QY 85 ELFGGNNMGLVAFVFGAALCAESVKNEMEPVGVQVDMVAVYLETRLADWTHSSGCV 144
 DB 130 ELFGVGVNMGRVAFVFGGVMCVSVNREMSPLVDNIATMTETLYLRHLNWIQDNGCV 189
 QY 145 AEFPLVGDGALBEARLRGNNASVTVLTGVALGALVTVGAFPSAK 193
 DB 190 DAFVELYGN-----SMRPLPFGFWSLXTLTLIS-LVLVAGCITLGVYLGHK 233
 RESULT 10
 BCL2_BOVIN STANDARD; PRT; 229 AA.
 ID BCL2_BOVIN
 AC 002718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RX MEDLINE=98162580; PubMed=9501056;
 RA Reyes R.A., Cockerell G.L.;
 RT "Increased ratio of bcl-2/bax expression is associated with bovine
 leukemia virus-induced leukemogenesis in cattle."
 RL Virology 242:184-192 (1998).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1) (by similarity).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2

domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RA-F-1 and TP53BP2 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).
 -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RA-F-1 (By similarity).
 -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
 -1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).
 -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 -1- SIMILARITY: Belongs to the Bcl-2 family.

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 EMBL: U92434; AAB5319.1; -
 DR HSSP: Q07817; 1MAZ.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl2_2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 KW DOMAIN 10 BH4.
 FT DOMAIN 64 68 POLY-PRO.
 FT DOMAIN 69 72 POLY-ALA.
 FT DOMAIN 83 97 BH3.
 FT DOMAIN 126 145 BH1.
 FT DOMAIN 177 192 BH2.
 FT TRANSMEM 202 223 POTENTIAL.
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
 FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 SQ SEQUENCE 229 AA; 25099 MW; ADIDDAF9EFPFLID CRC64;

Query Match 41.2%; Score 415.5; DB 1; Length 229;
 Best Local Similarity 38.2%; Pred. No. 4.2e-30;
 Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;

QY 9 DRRRAVADVGVKTLRGVYCGAG-----PGB----- 35
 DB 10 DRRRAVADVGVKTLRGVYCGAG-----PGB----- 35
 QY 36 ---GPAAD---LHOAMRAAGDEFTRFRTPSDIAOLHTVTPGAOCORFQVSDLEPQ 88
 DB 70 AAAGPAPSPVPVHLTLFGAGDDFRRRTRRDPAEMSSQHLTPFAARRERFATVDELR 129

QY 89 GPNWGRVIAVFFVFGALCAESVKNEMPLVGQVODMWAVYLETLADMISGGMABFT 148
 DB 130 DGVNMGRIAVFFRFGVGVCSVREMSPLVDSIALMTXETLNRHLHWIDNGMDAFV 189
 QY 149 ALYGDALBEARRLEGNWASVRTVLGVALGALVTVGAFPAK 193
 DB 190 ELYG---PSMRPLDFSMLSIKALLSLAL-VGACITLGAYLGHK 229
 RESULT 11
 ID BCL2 RAT STANDARD; PRT; 236 AA.
 AC P49950; 062837; 064032;
 DT 01-OCT-1996 (Rel. 34. Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94193015; PubMed=8144041;
 RA Sato T., Irie S., Krajewski S., Reed J.C.;
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
 RL Gene 140:291-292(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kenton M.W., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlmg messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 RN [3]
 RP SEQUENCE OF 19-172 FROM N.A.
 RX MEDLINE=95059917; PubMed=7969891;
 RA Castrén E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H., Lindholm D.;
 RT "bcl-2 messenger RNA is localized in neurons of the developing and adult rat brain.";
 RL Neuroscience 61:165-177(1994).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RA-F-1 and TP53BP2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RA-F-1 (By similarity).
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and

occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dpphosphorylated by protein phosphatase 2A (PP2A) (By similarity).

-1- PPM: Proteolytically cleaved by caspases during apoptotic cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-1- SIMILARITY: Belongs to the Bcl-2 family.

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DR EMBL: L14680; AAA53662.1; -

DR EMBL: U34964; AAA77687.1; -

DR PIR: I53744; I53744.

DR PIR: I67432; I67432.

DR HSP: Q07817; IMAZ.

DR InterPro: IPR000121; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; Bcl2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD RES 70 72 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT CONFLICT 42 42 A -> R (IN REF. 2).

FT CONFLICT 157 157 E -> G (IN REF. 2).

FT CONFLICT 164 164 S -> Y (IN REF. 2).

FT CONFLICT 212 212 L -> Q (IN REF. 2).

FT SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query Match 40.9%; Score 413; DB 1; Length 236;
Best Local Similarity 36.2%; Pred. No. 7,3e-30;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADGVGYKLRQKY----- 27

DB 10 DNRRIYMKYIHYKLSQSGYEMWDGDESDAPLAAPTGIFSGFQESNRTPAVHDTAART 69

QY 28 -----VCGAGRGSGPADPHQMRAGDEFRTFRFTPSDLAQHLVHTGSGAQQRPTQ 81

DB 70 SPLRPLVANNAGPASPVPVVLTLRRGGDFSRRYRDFEWSQHLTFTFARGPAT 129

QY 82 VSDRLFGGPMGRVLVAFVFGAALCAESVKNEMEPVGVQODVMVVALETRLDWIHS 141

DB 130 VVEELFRGVGVWGRIVAFERFGGVWCVSVREMSPLVDNIALMWTETLNHLHTWIDN 189

142 GGNMFPTALYGDGALBEARLRREGNMAVRTVLGVALGALVTGAFAPASK 193

DB 190 GGNDAFVELVIG-----PSMRPLPDSRWSLTKTLIAL-VAQCITLGVYLGKH 236

QY 142 GGNMFPTALYGDGALBEARLRREGNMAVRTVLGVALGALVTGAFAPASK 193

DB 190 GGNDAFVELVIG-----PSMRPLPDSRWSLTKTLIAL-VAQCITLGVYLGKH 236

RESULT 12

BCL2_MOUSE STANDARD; PRT; 236 AA.

ID BCL2_MOUSE

AC P10417; P10418;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2 OR BCL-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

[1]

SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

RC STRAIN=BAB/c; TISSUE=Liver;

RX MEDLINE=87187643; PubMed=3032455;

RA Negri M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;

RT "Molecular analysis of bcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";

RT Cell 49:455-463(1987).

RL [2]

REVIEWS TO 221-222.

RP MEDLINE=92375724; PubMed=1508712;

RX Eguchi Y., Swert D.L., Tsujimoto Y.;

RA "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RT Nucleic Acids Res. 20:4187-4192(1992).

RL [3]

PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

RP MEDLINE=92727291; PubMed=9115213;

RX Ito T., Deng X., Carr B., May W.S. Jr.;

RA "Bcl-2 phosphorylation required for anti-apoptosis function.";

RT J. Biol. Chem. 272:11671-11673(1997).

RL [4]

DEPHOSPHORYLATION BY PP2A.

RP MEDLINE=99069407; PubMed=9852076;

RX Deng X., Ito T., Carr B., Mundy M., May W.S. Jr.;

RA "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatine 1 is mediated by direct interaction with protein phosphatase 2A*.";

RT J. Biol. Chem. 273:34157-34163(1998).

RL [5]

FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Interacts with TP53BP2 (By similarity). Also interacts with APAF-1 and APAF-1.

CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=Alpha;

CC IsoId=P10417-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=P10417-2; Sequence=VSP_000513;

CC TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with APAF-1.

CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation

on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A).

-1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-1- SIMILARITY: Belongs to the Bcl-2 family.

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EMBL: U31532; AAA37282.1; -
DR EMBL: M16506; AAA37282.1; JOINED.
DR EMBL: M16506; AAA37281.1; -
DR PIR: B25960; TVMB31.
DR HSP: Q07817; IMAZ.
DR MGD: MGI:88138; Bcl2.
DR GO: GO:0005829; C:cytosol; IDA.
DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0006915; F:apoptosis; IDA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH4; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS0063; BH4_2; 1.
KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Phosphorylation.
KW Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC).
FT VARSPLIC 133 236 DAFVEYLGSMRPLFDPSLTKTLISLALVGACITLGLAYL
/FTID=VSP 000513.
/FTID=VSP 000513.
SQ SEQUENCE 236 AA; 26425 MW; AA85EF6B0766B0A CRC64;

Query Match 40.8%; Score 412; DB 1; Length 236;
Best Local Similarity 37.5%; Pred. No. 8; 9e-30;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRATADVGVKLRKGVVCGAG-----PG----- 34
Db 10 DREELVWKYTHKLSRGTEWMDGADADAPLGAAPTPGIFSPQPSNPVAVHREMAAT 69
QY 35 -----EGPAADP-----LHQAMRAAGDEFEETRRRTFSDLAQIHTVPGSAQOQRTQ 81
Db 70 SPLRLVATAGPALSLVPPCVHLTLRRADDTSRRYRRRPFAMSSQLHLTPETARGRFAT 129

QY 82 VSEDFGCGPMWGRVAFVFFGALCAESVKNEMEPVGVQVDMVAVYLETRADWISS 141
Db 130 VVEELFPGVAMGRVAFVFFGCGVNCVSVREMSPLVDNIALMWTETLNRHLHWIQDN 189
QY 142 GGMWAFETALYGDGALGEARLRREGWASVRIVLTGVALGALVTVGAFFPASK 193
Db 190 GGMWDAFVELYG----PSMRPLFDPSLTKTLISLAL-VGACITLGLAYLGHK 236

RESULT 13
BCL2 HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q13842; Q16197;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Teujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Teujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) cell translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-1g fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.
RX MEDLINE=88196071; PubMed=2834197;
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson F.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hooten R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sotergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
 RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
 RX MEDLINE=92096610; PubMed=1339299;
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.,
 RT "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 RN [8]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=91066924; PubMed=2250705;
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.,
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 RN [9]
 RP MUTAGENESIS.
 RX MEDLINE=94239528; PubMed=8183370;
 RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.,
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 RN [10]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
 RX MEDLINE=98057466; PubMed=9395403;
 RA Cheng E.H.-Y., Kitzsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
 RA Ueno K., Hardwick J.M.,
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
 RL Science 278:1966-1968(1997).
 RN [11]
 RP INTERACTION WITH TP53BP2.
 RX MEDLINE=96251339; PubMed=8668206;
 RA Namovsek L., Cleary M.L.,
 RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes
 RT cell cycle progression at G2/M.";
 RL Mol. Cell. Biol. 16:3884-3892(1996).
 RN [12]
 RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE=21260650; PubMed=11368354;
 RA Ruvolo P.P., Deng X., May W.S.,
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
 RL Leukemia 15:515-522(2001).
 RN [13]
 RP PHOSPHORYLATION BY ASK1/JNK1.
 RX MEDLINE=20036804; PubMed=10567572;
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.,
 RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
 RT protein kinase pathway normally activated at G(2)/M.";
 RL Mol. Cell. Biol. 19:8469-8478(1999).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (Apaf-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2
 CC domains, and is necessary for anti-apoptotic activity (by
 CC similarity). Also interacts with APAF-1, RAIF-1 and TP53BP2.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=PI0415-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=PI0415-2; Sequence=VSP 000512;
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAIF-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
 CC II chronic lymphatic leukemia) by a chromosomal translocation
 CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
 CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
 CC the chromosomal translocation could be attributed to the Ig
 CC somatic hypermutation mechanism resulting in nucleotide
 CC transfections.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.inbiohogen.fr/services/chromocancer/gene/BCL2ID49.html".
 CC
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 CC
 CC -----
 CC EMBL: M13994; AAAS1813.1; ALT_SEQ.
 CC EMBL: M13995; AAAS1814.1; ALT_SEQ.
 CC EMBL: M14745; AAA35591.1; -
 CC EMBL: X06487; CAA29778.1; -
 CC EMBL: AY220759; AAO26045.1; -
 CC EMBL: BC027258; AAO27258.1; -
 CC EMBL: S72602; AAD14111.1; ALT_SEQ.
 CC PIR: B29409; TVHUB1.
 CC PIR: C37332; TVHUA1.
 CC PDB: 1G5W; 2I-MAR-01.
 CC PDB: 1GJH; 13-JUN-01.
 CC GeneW: HGNC:990; BCL2.
 CC MIM: 151430; -
 CC DR GO: GO:0005743; C:mitochondrial inner membrane; TAS.
 CC DR GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
 CC DR GO: GO:0006916; F:anti-apoptosis; TAS.
 CC DR GO: GO:0006959; P:humoral immune response; TAS.
 CC DR GO: GO:0008285; P:regulation of cell cycle; TAS.
 CC DR GO: GO:000074; P:regulation of cell proliferation; TAS.
 CC DR InterPro: IPR000712; Bcl2_BH.
 CC DR InterPro: IPR003093; Bcl2_BH4.
 CC DR InterPro: IPR002475; Bcl2_family.
 CC DR InterPro: IPR004725; Bcl2_reg.
 CC
 CC Query Match 40.8%; Score 411.5; DB 1; Length 229;
 CC Best Local Similarity 37.0%; Pred. NO. 1e-29;
 CC Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;
 CC 9 DTRALVADPFYGYKLRQKGYCGAG-----PGE----- 35

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Db 10 DNREIWMKYIHYKLSQREYMDAGDVGAAPGAAAPGIFSSQSGHTHPAASRDVPVART 69
QY 36 -----GPAADP-----LHQAMRAAGDEPFRPTFRPSDLAQLHTVPGSAOOR 78
Db 70 SPLQTPAAPGAAAGALSPVPVVLTLRQADDLSKRRYRDFAMSSQLHTPTTARGR 129
QY 79 FTOVSDLEFQGGPMNRLVAFVFGAALCAESVKNEMBEVLGVQODVMVAVLETRLADMI 138
Db 130 FATVVEELFRQGVNMGRIYAFPEFGVNCVBSVNRMSPLVDNIALMTETYLNRHLHTMI 189
QY 139 HSSGGMAEFTALYGCALBEARLRREGNMASTRVTLTGAVALGVTVGAFPAASK 193
Db 190 QDNQGMDFVELYG-----PSMRPLDFPSMLSLKTLISLAL-VGACITIGAYLGHK 239

RESULT 14
BCL2_CRILO STANDARD; PRT; 236 AA.
AC Q9JUV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxId=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA MEDLINE=20431763; PubMed=10973819;
RT Tonicic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RA MEDLINE=21092839; PubMed=11181062;
RT Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAIF-1 and TP53BP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAIF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -1- PM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

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CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC -----
CC EMBL: AJ271720; CAB92245.1; -.
CC PIR: J07383; J07383.
CC HSSP: O07817; IMA2.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; Bcl2_family.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2_1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRFAMs: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS50063; BH4_2; 1.
CC DR PROSITE: PS50063; BH4_2; 1.
CC KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT MOD RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 236 AA; 26491 MW; BECADPFEF337228 CRC64;

Query Match 39.8%; Score 402; DB 1; Length 236;
Best Local Similarity 35.3%; Freq. No. 7e-29;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADFVGVYKRLQKGY----- 27
Db 10 DNREIWMKYIHYKLSQREYMDAGDVGAAPGAAAPGIFSSQSGHTHPAASRDVPVART 69
QY 28 -----VCGAGPREGPAADPLHQAMRAAGDEPFRPTFRPSDLAQLHTVPGSAOORFTQ 81
Db 70 SPLRPIVATVGTGPTLSPVPVVLTLRQADDLSKRRYRDFAMSSQLHTPTTARGRPAT 129
QY 82 VSDELFGQGGPMNRLVAFVFGAALCAESVKNEMBEVLGVQODVMVAVLETRLADMISS 141
Db 130 VEEELFRQGVNMGRIYAFPEFGVNCVBSVNRMSPLVDNIALMTETYLNRHLHTMIODN 189
QY 142 GGMAEFTALYGCALBEARLRREGNMASTRVTLTGAVALGVTVGAFPAASK 193
Db 190 QDNQGMDFVELYG-----PSMRPLDFPSMLSLKTLISLAL-VGACITIGAYLGHK 239

RESULT 15
AR1_XENLA STANDARD; PRT; 204 AA.
AC 091828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator R11 (XR11).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.

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RX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RL cell-survival genes.";
RL Gene 158:171-179(1995).
CC - FUNCTION: Confers strong protection against cell death.
CC - SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC - DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC - SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC - SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC - SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X82461, CAA57844.1, -.
DR HSSP, Q07817, IMXZ.
DR InterPro, IPR000712, Bcl2_BH.
DR InterPro, IPR003093, Bcl2_BH4.
DR InterPro, IPR002475, Bcl2_family.
DR InterPro, IPR004725, Bcl2_reg.
DR Pfam, PF00452, Bcl-2_1.
DR Pfam, PF02180, BH4_1.
DR SMART, SM00337, BCL_1.
DR SMART, SM00265, BH4_1.
DR TIGRFAMs, TIGR00865, bcl-2_1.
DR PROSITE, PS01080, BH1_1.
DR PROSITE, PS01258, BH2_1.
DR PROSITE, PS50062, BCL2_FAMILY_1.
KW Apoptosis; Transmembrane.
KW DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SO SEQUENCE 204 AA; 23379 MW; 3BFC6EB6DDA4CA03 CRC64;

Query Match 36.6%; Score 369; DB 1; Length 204;
Best Local Similarity 42.1%; Pred. No. 5,3e-26;
Matches 82; Conservative 24; Mismatches 63; Indels 26; Gaps 4,

OY 10 TRALVADVVGYKLRKQGVYC-----GAGPGGGPAADPHOMKR 47
DB 5 SRDLVEKVSXKLGS-NEACRKFSNNPNMPLYMEPTSERBEGATGTIVEEVLQLL 63
OY AAGDEFETFRPRTFSDLAOLHTVPFGSAOORFTOVSDLEFOCGPMWRGLVAFFVGALC 107
DB 64 EATEFEELRYQRAFESDLSQLHITDPTIAQOSIQVMGELFRGCTWGWIVAFSFGRLC 123
OY 108 AESVNKEMEPLVGVQVDMMVAVYLETRLADWIHSGGMAFTALYGDALAEARRLRE--G 165
DB 124 VESANKENTDLLPRIVQMVMNVNLTHTLPQMWQENGCEAWFGLYKNAAGAQRSEGRFG 183
OY 166 NWASIVRVLTGAVAL 180
DB 184 RLTLTI-VMLTGVFAL 197

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Search completed: February 26, 2004, 11:13:30
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:10:37 / Search time 45 Seconds
(without alignments)
1353.223 Million cell updates/sec

Title: US-09-508-745-4
Perfect score: 1009

Sequence: 1 MATPASPDPDRALVADPVG.....LTGAVLALGVTVGAFPAASK 193

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1005	99.6	193	11	O88996 ratius norv
2	1005	99.6	219	11	O7TS60 ratius norv
3	965	95.6	193	11	O8CG14 mus musculu
4	770	76.3	178	11	O9CWM5 mus musculu
5	770	76.3	178	11	O8CFR2 mus musculu
6	439.5	43.6	233	6	O9MYW4 oryctolagus
7	435.5	43.2	233	11	O35844 mus musculu
8	432.5	42.8	233	6	O8SQ42 felis silve
9	431.5	42.8	233	6	O9N1A2 sus scrofa
10	428.5	42.5	233	6	O9MZS7 ovis aries
11	412	40.8	236	11	O8BQK4 mus musculu
12	412	40.8	236	11	O7TSN8 ratius norv
13	406	40.2	79	11	O7TS61 ratius norv
14	401	39.7	180	6	O9BD5 bos taurus
15	401	39.7	217	11	O9N35 mus musculu
16	400	39.6	238	13	O90298 brachydanio

17	398.5	39.5	180	6	O9BDX7	O9bdx7 bos taurus
18	398	39.4	236	11	O923R6	O923r6 cricetus
19	395.5	39.2	235	6	O8I008	O8i008 felis silve
20	380.5	37.7	284	11	O7TS62	O7ts62 ratius norv
21	374.5	37.1	188	11	O9QWX2	O9qwx2 mus musculu
22	374.5	37.1	235	11	O35843	O35843 mus musculu
23	372.5	36.9	188	4	O9H1R6	O9h1r6 homo sapien
24	371	36.8	204	13	O90ZH2	O90zh2 xenopus lae
25	365.5	36.2	153	6	O7YR86	O7yr86 canis famli
26	353	35.0	185	6	O8M3B1	O8mj81 bos taurus
27	347	34.4	219	11	O99N36	O99n36 mus musculu
28	342.5	33.9	199	11	O8C5P0	O8c5p0 mus musculu
29	296	29.3	89	13	O8UWJ1	O8uwj1 gallus gall
30	187	18.5	209	11	O9UK59	O9uk59 ratius norv
31	185	18.3	170	11	O9WU15	O9wu15 ratius norv
32	182	18.0	209	11	O8C264	O8c264 mus musculu
33	174.5	17.3	192	13	O919N4	O919n4 brachydanio
34	172.5	17.1	221	13	O98U13	O98u13 xenopus lae
35	170.5	16.9	190	4	O8NFP3	O8nft3 homo sapien
36	168.5	16.7	125	4	O9H1R5	O9h1r5 homo sapien
37	163	16.2	235	5	O967D2	O967d2 geodia cydo
38	162	16.1	38	11	O9R1B3	O9r1b3 ratius norv
39	157.5	15.6	163	6	O9MZS6	O9mz86 ovis aries
40	156.5	15.5	173	11	O8K3J2	O8k3j2 mus musculu
41	154	15.3	173	4	O8W249	O8w249 homo sapien
42	154	15.3	173	11	O9UKL3	O9ukl3 ratius norv
43	151	15.0	67	6	O8M3B3	O8mj83 cervus elap
44	149	14.8	192	6	O8SQ43	O8sq43 felis silve
45	148.5	14.7	218	5	O9N754	O9n754 suberites d

ALIGNMENTS

RESULT 1

O88996 PRELIMINARY; PRT; 193 AA.

AC O88996; (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Bcl-w.

GN BCL-W.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=99292146; PubMed=1036024;

RA Hammer S., Skoglosa Y., Lindholm D.,

RT "Differential expression of bcl-w and bcl-x messenger RNA in the

RT developing and adult rat nervous system.";

RL Neuroscience 91:673-684(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=22672518; PubMed=12787069;

RA Itoh T., Itoh A., Pleasure D.,

RT "Bcl-2-related protein family gene expression during oligodendroglial

RT differentiation.";

RL J. Neurochem. 85:1500-1512(2003).

DR EMBL; AF096291; AAC64200.1; -.

DR HSSP; O07817; IMAZ.

DR GO; GO:0016329; F:apoptosis regulator activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 193;
 Best Local Similarity 99.5%; Pred. No. 3.9e-81;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60
 DB 1 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 QY 121 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 180
 DB 121 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193

RESULT 2

QY 07TS60 PRELIMINARY; PRT; 219 AA.
 AC 07TS60;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE BCL-WEL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 differentiation";
 RT EMBL; AY185100; AA064470.1; --
 DR EMBL; AY185100; AA064470.1; --
 SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 219;
 Best Local Similarity 99.5%; Pred. No. 4.6e-81;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60
 DB 27 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 86
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 QY 87 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 146
 DB 121 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 180
 DB 147 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 206
 QY 181 GALVTVGAFPAASK 193
 DB 207 GALVTVGAFPAASK 219

RESULT 3
 O8CGL4 PRELIMINARY; PRT; 193 AA.

ID O8CGL4
 AC O8CGL4;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bcl2-like protein 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL; TISSUE=Skin;
 RA Su H.-Y.;
 RT "Extraction from neonatal mouse skin after IGF-1 stimulation."
 RT Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY170344; AA013177.1; --
 DR MGD; MGI:108052; Bcl2l2.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 SQ SEQUENCE 193 AA; 20950 MW; 258AC181B16DFA0 CRC64;

Query Match 95.6%; Score 965; DB 11; Length 193;
 Best Local Similarity 96.4%; Pred. No. 1.4e-77;
 Matches 186; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60
 DB 1 MATPASTPTDTRALVADPFVGYKLRQKGYVCGAGPGEGPADPLHQMRAAGDEFETRFRRT 60
 QY 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 DB 61 FSDLAAGLHVTPGSAQQRFTQVSDELFGCGPWNMGRVAFVFGALCAESVNKEMEPVVG 120
 QY 121 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 180
 DB 121 QVQDMWVAVLETRLDWTHSSGMAEFPTALYGDGALBEARRLRBNWNASVRTVLGAVALL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193

RESULT 4

QY 09CYW5 PRELIMINARY; PRT; 178 AA.
 AC 09CYW5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 24, Last annotation update)
 DE Bcl2-like 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kocha H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,
 RA Schiraldi L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okide T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hoffmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaers P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 DR EMBL; AK013244; BAB28740.1; -.
 DR HSSP; Q07817; IMAZ.
 DR MGD; MGI:108052; Bcl2l2.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR002475; Bcl2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 178 AA; 19147 MW; E2D4CF79528E9D7 CRC64;
 Query Match 76.3%; Score 770; DB 11; Length 178;
 Best Local Similarity 96.7%; Pred. No. 2.3e-60;
 Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60
 DB 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60
 QY 61 FSDLAQLHTPGSAQGRFTQVSDLEPQGGPNMGRVAFVFGALCAESYKMEPLVG 120
 DB 61 FSDLAQLHTPGSAQGRFTQVSDLEPQGGPNMGRVAFVFGALCAESYKMEPLVG 120
 QY 121 QVQDMVAVLETRLADWIHSSGGWAEFTAL 150
 DB 121 QVQDMVAVLETRLADWIHSSGGWAEFTAL 150
 RESULT 5
 Q8CER2 PRELIMINARY; PRT; 178 AA.
 AC Q8CER2; PRELIMINARY; PRT; 178 AA.
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Bcl2-1ike 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strauberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040369; AAH40369.1; -.
 DR MGD; MGI:108052; Bcl2l2.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; BCL2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;
 Query Match 76.3%; Score 770; DB 11; Length 178;
 Best Local Similarity 96.7%; Pred. No. 2.3e-60;
 Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60
 DB 1 MATPASTPDRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRRRT 60
 QY 61 FSDLAQLHTPGSAQGRFTQVSDLEPQGGPNMGRVAFVFGALCAESYKMEPLVG 120
 DB 61 FSDLAQLHTPGSAQGRFTQVSDLEPQGGPNMGRVAFVFGALCAESYKMEPLVG 120
 QY 121 QVQDMVAVLETRLADWIHSSGGWAEFTAL 150
 DB 121 QVQDMVAVLETRLADWIHSSGGWAEFTAL 150
 RESULT 6
 Q9MYW4 PRELIMINARY; PRT; 233 AA.
 AC Q9MYW4; PRELIMINARY; PRT; 233 AA.
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Bcl-X.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knott J.C., Robertson L., James E.R.;
 RT "Rabbit Bcl-X";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY005131; AAF88137.1; -.
 DR HSSP; P53563; IAF3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; BCL2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match Similarity      43.6%; Score 439.5; DB 6; Length 233;
Best Local Similarity       42.0%; Pred.No.5,9e-31;
Matches   94; Conservative    22; Mismatches  57; Indels   51; Gaps     4

QY          11 PALVADPFYGKLRGKYVC-----GAG-----PGRGPA 39
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB          6 RELVVDPFLSTYKSQGYSMSCFSDVEENRTEAPEEGTPEMETPSAINGNPAMHPADS PAV 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY          40 D-----PLHQMPRAAGDEFTFRRTFSSLLAQHAYTPSAQCGRPTQ 81
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB         66 NGATGHSSSLDAREVI PMTVAKQAALREAGDEFELRYRAFSDLTSQLHTPPGA YQS FEO 125
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY        VSDLEFOGGPMMGRVLVAFPVFCAALCAESVNKEMLVGQVDWMWAYJETRLADMHS 141
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB       126 VNNELFRCGVNMGRI VAFFSFGCALCVSEVDXEMEYLVSRIAAMNTIYNDLHFPIQEN 185
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY        142 GGWAETLALYGDGDALEARRLRE--GNMA SVRTLGTAVAVALGAL 183
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       186 GMWTFVELYGNNAAAESHKRGERFNRPFLTGMTVAAGVLLGLSL 229
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
O35844 ID O35844 PRELIMINARY; PRT; 233 AA.
O35844 AC O35844;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bcl-xL.
DN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RP STRAIN=B6/CBA; TISSUE=Thymus;
RC MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-X isoform connected to the T cell receptor regulatess apoptosis in T cells.";
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -.
DR HSSSP; P53563; IAF3.
DR MGI; MG1-88139; Bcl2l.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016325; F:apoptosis regulator activity; IEA.
DR DR GO:0006915; P:apoptosis; IEA.
DR InterPro; IPRO00712; Bcl2 BH.
DR InterPro; IPRO03093; Bcl2 BH4.
DR InterPro; IPRO02475; Bcl2_family.
DR InterPro; IPRO04725; Bcl2_reg.
DR Pfam; PF00452; Bcl_2; 1.
DR Pfam; SMO0337; BCL; 1.
DR SMART; SMO0265; BH4; 1.
DR TIGRFAMS; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083FP2D8327E072E CRC64;
```

QY	CGAGPBGPAAD-----PLHQMRAAGDEFERPRRTTSDLAQTLHTYTPSAOORFT	80
Db	66 NGA-TGHSSSLDAREVYIPMAAAYKQALREAGDEFEIRTRAPASDLTSLQHTTPGAYOSFE	124
QY	81 QVSDLEFQCGPWPWGRVLVAFVFGAALCAESVYKMEPELVGVQVDDMYAVYLETRLDWYHS	140
Db	125 QVYNLEFPRGVAVWGRIVAFVFSFGALCVESYDKEMQVLYVRSIAWMATYINDHLEPIQE	184
QY	141 SGGWAEFTALYDGDALREARLRGEG--NWASVRYTLTGAVAGAL	183
Db	185 NGMDTFVLDLYGNNAABSRKKEGFRNRFPTGMTVAGVLLGSL	229
RESULT 8		
Q8SQ42		
Q8SQ42	PRELIMINARY; PRT; 233 AA.	
AC	Q8SQ42;	
DT	01-JUN-2002 (T-EMBLrel. 21, Created)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)	
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)	
DE	Bcl-XL protein.	
GN	BCL-XL.	
OS	Felis silvestris catus (Cat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.	
OX	NCBI_TaxID=9685;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Nagafuchi S., Sano J., Kano R., Hasegawa A.;	
RT	"Molecular cloning of feline Bcl-2 family.";	
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.	
DR	EMBL; AB080951; BAB85856.2; -	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.	
DR	GO; GO:0006915; P:apoptosis; IEA.	
DR	InterPro; IPR000712; Bcl2_BH.	
DR	InterPro; IPR003093; Bcl2_BH4.	
DR	InterPro; IPR002475; BCL2_Family.	
DR	InterPro; IPR004725; Bcl2_reg.	
DR	Pfam; PF00452; Bcl-2; 1.	
DR	Pfam; PF02180; BH4; 1.	
DR	SMART; SM00337; BCL; 1.	
DR	SMART; SM00265; BH4; 1.	
DR	TIGRFAMs; TIGR00865; bcl-2; 1.	
DR	PROSITE; PSS0062; BCL2_FAMILY; 1.	
DR	PROSITE; PS01080; BH1; 1.	
DR	PROSITE; PS01258; BH2; 1.	
DR	PROSITE; PS01259; BH3; 1.	
DR	PROSITE; PS01260; BH4_1; 1.	
DR	PROSITE; PSS0063; BH4_2; 1.	
DR	SEQUENCE 233 AA; 26017 MW; CD1724F59D47BC9 CRC64;	
Query Match 42.9%; Score 432.5; DB 6; Length 233;		
Best Local Similarity 41.6%; Pred. No. 2.5e-30;		
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5		
QY	11 RALVAVFYGYKRYKRGY-----Y 28	
Db	6 RELVVDLFYLYKLSQKGYGMSRPSVDEENKRTAPGCTSEMETPBAINGNPSMHLADSPAY 65	
QY	29 CGAGPBGPAAD-----PLHQMRAAGDEFETRRRTTSDLAQTLHTYTPSAOORFT 80	
Db	66 NGA-TGHSSSLDAREVYIPMAAAYKQALREAGDEFEIRTRAPASDLTSLQHTTPGAYOSFE 124	
QY	81 QVSDLEFQCGPWPWGRVLVAFVFGAALCAESVYKMEPELVGVQVDDMYAVYLETRLDWYHS 140	
Db	125 QVYNLEFPRGVAVWGRIVAFVFSFGALCVESYDKEMQVLYVRSIAWMATYINDHLEPIQE 184	
QY	141 SGGWAEFTALYDGDALREARLRGEG--NWASVRYTLTGAVAGALVTVGAFFASK 193	
Db	185 NGMDTFVLDLYGNNAABSRK--GQERSNWFLLTGMTVAG-VVLGSLPSRK 233	

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RESULT 9
ID Q9N1A2 PRELIMINARY; PRT; 233 AA.
AC Q9N1A2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Anti-apoptotic regulator Bcl-XL.
GN BCL-XL.
OS Sus scrofa (Pig) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lee T.L., Canty J.M.;
RT "PCR Cloning of a Porcine bcl-xl cDNA from Heart.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216205; AAF3212.1; -.
DR HSSP; Q07817; IMAZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR003093; BCL2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; BCL2_reg.
DR Pfam; PF00452; BCL-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.8%; Score 431.5; DB 6; Length 233;
Best Local Similarity 41.8%; Pred. No. 3e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKYLROKGY-----V 28
DB 6 RELVVDPLSTKLSQKGSWSQFTVEENRTAEPTGTESEATPSPAINGNPSMHLADSPAV 65
QY 29 CGAGPGECPAD-----PLHQAMRAAGDEFETFRFRTPSDLAQLHVTGSAQORFT 80
DB 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRARSDDLTSQHLITPGTAQSFE 124
QY 81 QVSDLEFGCGPGRWGLVAFVFPFGAALCAESVKNKMEPLVGVQVQMMVAYLERLADWTHS 140
DB 125 QVNNELFRDGVNMGRIIVAFVFPFGALCVESVDKEMQVIVSRITATWMAIYLDHLEPWIOE 184
QY 141 SGGAAEFATLYGDGALREARLRE--GNWASVRTVLTGAVVALGAL 183
DB 185 NGMDTFVELYGNNAAESRKQGERFRNRFMTGNTLACVAVLLGSL 229

RESULT 10
ID Q9WZS7 PRELIMINARY; PRT; 233 AA.
AC Q9WZS7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bcl-x long protein.
OS Ovis aries (Sheep) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bcl-x in the sheep ovary.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164517; AAF89532.1; -.
DR HSSP; P53563; IAF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR003093; BCL2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; BCL-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26134 MW; 012BPA1382762915 CRC64;

Query Match 42.5%; Score 428.5; DB 6; Length 233;
Best Local Similarity 40.6%; Pred. No. 5.6e-30;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKYLROKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVVDPLSTKLSQKGSWSQFSDVEENRTAEPTGTESEATPSPAINGNPSMHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRFRTPSDLAQLHVTGSAQORFTQ 81
DB 66 NGATGHSRSLDAREVLPMAAVKQALREAGDEFELRYRARSDDLTSQHLITPGTAQSFEQ 125
QY 82 VSDLEFGCGPGRWGLVAFVFPFGAALCAESVKNKMEPLVGVQVQMMVAYLERLADWTHS 141
DB 126 VNNELFRDGVNMGRIIVAFVFPFGALCVESVDKEMQVIVSRITATWMAIYLDHLEPWIOE 185
QY 142 GGMAEFTALYGDGALREARLRE--GNWASVRTVLTGAVVALGAL 183
DB 186 GGMDTFVELYGNNAAESRKQGERFRNRFMTGNTVAGVALLGSL 229

RESULT 11
ID Q8BOK4 PRELIMINARY; PRT; 236 AA.
AC Q8BOK4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE B-cell leukemia/lymphoma 2.
GN BCL2.
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";

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DR InterPro: IPR000712; BCL2_BH.
 DR InterPro: IPR002475; BCL2_family.
 DR Pfam: PF00452; BCL2_1.
 DR SMART: SM00337; BCL_1.
 DR PROSITE: PS00662; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 180 AA; 20062 MM; 95DC436F95DABDAE CRC64;

Query March 39.7%; Score 401; DB 6; Length 180;
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEPETERRRRTFSDDLAQLHVTGSAQORFTQVSDLELFCGSPNMGRLVAFVFG 103
 DB 38 QALREAGDEPFLRRRAFSDLTSLHTPGTAYQSPFQVNVNELPRDGVNMGRIVAFSFG 97
 QY 104 AALCAESYNKEMEPVGVQVDMVAVYETRLADMIHSSGWAFTALYGDALBEARLR 163
 DB 98 GALTVESVDKEMQVLVSRIATWMTYLDHLEPMIOENGWDTFVELYGNNAAESRRKQ 157
 QY 164 E-GNMA5VRTVLTGAVALLGAL 183
 DB 158 ERFNRWFLTGMTVAGVLLGSL 179

RESULT 15

ID Q99N35 PRELIMINARY; PRT; 217 AA.
 AC Q99N35;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE B-cell leukemia/lymphoma x (Fragment).
 GN BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Yang X.-F., Cantor H.;
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory
 gene Bcl-x-gamma."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF133282; AAK15455.1; -
 DR EMBL: AF133281; AAK15455.1; JOINED.
 DR HSSP: P53563; IAF3.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO: GO:0006915; P:apoptosis; IEA.
 DR InterPro: IPR00712; BCL2_BH.
 DR InterPro: IPR00475; BCL2_family.
 DR Pfam: PF00452; BCL2_1.
 DR SMART: SM00337; BCL_1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE: PS00662; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 217 AA; 24234 MM; 3B5A4E09A7DEF18 CRC64;

Query Match 39.7%; Score 401; DB 11; Length 217;
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEPETERRRRTFSDDLAQLHVTGSAQORFTQVSDLELFCGSPNMGRLVAFVFG 103

DB 72 QALREAGDEPFLRRRAFSDLTSLHTPGTAYQSPFQVNVNELPRDGVNMGRIVAFSFG 131
 QY 104 AALCAESYNKEMEPVGVQVDMVAVYETRLADMIHSSGWAFTALYGDALBEARLR 163
 DB 132 GALTVESVDKEMQVLVSRIATWMTYLDHLEPMIOENGWDTFVDLYGNNAAESRRKQ 191
 QY 164 E-GNMA5VRTVLTGAVALLGAL 183
 DB 192 ERFNRWFLTGMTVAGVLLGSL 213

Search completed: February 26, 2004, 11:14:31
 Job time : 50 secs

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